OM protein - protein search, using sw model

Run on: February 8, 2006, 03:09:18 ; Search time 200 Seconds
274.612 Million cell updates/sec
(without alignments)

GenCore version 5.1.7
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Title: US-10-661-784-2
Perfect score: 670
Sequence: 1 GSGKDPVQPPTKICVGCPRD..........YVVPWEKKIYPTVNCQPLGM 125

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_21:*
            1: geneseqp1980s:*
            2: geneseqp1990s:*
            3: geneseqp2000s:*
            4: geneseqp2001s:*
            5: geneseqp2002s:*
            6: geneseqp2003s:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
            9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670	100.0	125	8	ADM16603	HK-D3v (GS
2	670	100.0	125	9	ADY71957	Variant h
3	660	98.5	123	3	AAY95426	Human hig
4	660	98.5	123	8	ADM16602	Native HK
5	660	98.5	123	9	ADY71956	Native hu
6	660	98.5	268	8	ADP43683	Human PMM
7	660	98.5	268	6	ABM83721	Human dia
8	660	98.5	304	8	ABP70801	Human ext
9	660	98.5	304	6	ABP70801	Human ext
10	660	98.5	322	8	ABM83720	Human dia
11	660	98.5	326	8	ABP70799	Human ext
12	660	98.5	329	6	ABM83717	Human dia
13	660	98.5	329	6	ABM83716	Human pro
14	660	98.5	358	6	ABP70800	Human ext
15	660	98.5	362	9	AEB32339	Human pro
16	660	98.5	362	6	AEB32341	Human pro
17	660	98.5	390	8	ABU99149	Novel hum
18	660	98.5	390	6	ADM93863	Human NOV
19	660	98.5	390	6	ABU99149	Novel hum
20	660	98.5	390	6	ADT04032	Novel hum
21	660	98.5	392	6	ADS93172	Novel hum
22	660	98.5	390	8	ABM83719	Human dia
23	660	98.5	398	8	ABU99143	Human hum
24	660	98.5	398	8	ADM93851	Human NOV
25	660	98.5	398	8	ABM83718	Human dia
26	660	98.5	398	8	ADS93160	Novel hum
27	660	98.5	427	8	ADE76864	Human pro
28	660	98.5	427	8	ABM83715	Human dia
29	660	98.5	427	8	ABM80523	Tumour-as
30	660	98.5	427	8	ADQ39518	Human myo
31	660	98.5	427	8	ADQ39516	Human myo
32	660	98.5	579	9	ADS93164	Novel hum
33	660	98.5	579	8	AEB32342	Human pro
34	660	98.5	612	8	AEB32338	Human pro
35	660	98.5	615	6	ADS93142	Novel hum
36	660	98.5	615	8	ABU99144	Novel hum
37	660	98.5	616	8	ADM93853	Human NOV
38	660	98.5	621	8	ADS93162	Novel hum
39	660	98.5	621	8	ADS93154	Novel hum
40	660	98.5	621	8	ADS93156	Novel hum
41	660	98.5	622	5	ADS93184	Novel hum
42	660	98.5	626	8	ADS93158	Novel hum
43	660	98.5	626	8	ABB78707	Novel hum
44	660	98.5	644	4	ABG21101	Novel hum
45	660	98.5	644	5	ABB78710	Human hig

ALIGNMENTS

RESULT 1

ID   ADM16603 standard; protein; 125 AA.
XX
AC   ADM16603;
XX
DT   17-JUN-2004 (first entry)
XX
DE   HK-D3v(GS) amino acid sequence, seq id 2.
XX
KW   Cytostatic; nootropic; neuroprotective; antiparkinsonian; inhibitor;
KW   cell migration; cell invasion; cell proliferation; angiogenesis;
KW   apoptosis; tumour growth rate; human kininogen domain 3v; HK-D3;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   amyotrophic lateral sclerosis; ALS; mutein.
OS   Homo sapiens.
OS   Synthetic.
XX
XX
PN   WO2004024877-A2.
XX
PD   25-MAR-2004.
XX
PF   15-SEP-2003; 2003WO-US028881.
XX
PR   13-SEP-2002; 2002US-0410279P.
XX
PA   (ATTE-) ATTENUON LLC.
XX
PI   Donate F, Mazar A;
XX
DR   WPI; 2004-270022/25.
DR   N-PSDB; ADM16606.
XX
PT   Novel isolated anti-angiogenic polypeptide comprising sequence of human
PT   kininogen domain 3v (HK-D3v) or variant of native HK-D3, useful for
PT   inhibiting angiogenesis, endothelial cell proliferation or endothelial
PT   tube formation.
XX
PS   Disclosure; SEQ ID NO 2; 79pp; English.
XX
CC   The invention relates to an isolated anti-angiogenic polypeptide (I)
CC   comprising the sequence of human kininogen domain 3v (HK-D3v) (fully
CC   defined sequence (S1) of 127 amino acids as given in specification) or
CC   variant or derivative of native HK-D3 (fully defined sequence (S2) of 123
CC   amino acids as given in specification), and has at least 20% of activity
CC   of native HK-D3 in inhibiting angiogenesis, endothelial cell

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CC   proliferation or endothelial tube formation. Also disclosed is a
CC   diagnostically or therapeutically labelled anti-angiogenic polypeptide
CC   (II) comprising (I) labelled with a diagnostic or therapeutic label, and
CC   a diagnostic HK-D3-related composition (III) comprising (II) labelled
CC   with a detectable label and a carrier. Further disclosed is an affinity
CC   ligand (IX) useful for binding to or isolating an HK-D3-binding molecule
CC   or cells expressing the binding molecule, comprising (I) immobilized to a
CC   solid support or carrier. (I) or (II) are useful for inhibiting cell
CC   migration, cell invasion, cell proliferation or angiogenesis, or for
CC   inducing apoptosis which involves contacting cells associated with
CC   undesired cell migration, invasion, proliferation or angiogenesis with
CC   (I). (I) is useful for treating neurodegenerative diseases e.g.,
CC   Alzheimer's disease, Parkinson's disease or amyotrophic lateral sclerosis
CC   (ALS). The current sequence represents an N-terminal addition variant of
CC   HK-D3 designated HD-D3v(GS), that includes an additional GS at the N-
CC   terminus.
XX
SQ   Sequence 125 AA;

Qy   Best Match
     Query Match          100.0%;  Score 670;  DB 8;  Length 125;
     Best Local Similarity 100.0%;  Pred. No. 3.3e-67;
     Matches  125;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ 60

Qy   61 VVAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120

Qy  121 QPLGM 125
         |||||
Db  121 QPLGM 125
```

RESULT 2

```
ID   ADY71957
AC   ADY71957 standard; protein; 125 AA.
XX
AC   ADY71957;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Variant human kininogen domain 3 Hk-D3v(GS) protein.
XX
KW   protein engineering; kininogen; antiangiogenic; apoptosis; angiogenesis;
KW   cancer; cytostatic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US20050058599-A1.
XX
PD   17-MAR-2005.
XX
PF   15-SEP-2003; 2003US-0061784.
XX
PR   15-SEP-2003; 2003US-0061784.
XX
PA   (DONA/) DONATE F.
PA   (MAZA/) MAZAR A P.
XX
PI   Donate F, Mazar AP;
XX
PT   Novel human kininogen domain 3 variant inhibiting angiogenesis,
PT   endothelial cell proliferation or endothelial tube formation, useful for
PT   treating disease associated with undesired cell migration, invasion,
PT   proliferation or angiogenesis.
XX
DR   WPI; 2005-213544/22.
DR   N-PSDB; ADY71960.
XX
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```
PS   Disclosure; SEQ ID NO 2; 35pp; English.
XX
CC   The invention relates to an isolated anti-antiangiogenic polypeptide (I)
CC   having the sequence of human kininogen domain 3 variant (HK-D3v) having a
CC   fully defined 127 amino acid sequence given in the specification, or its
CC   variant or derivative of native HK-D3 having a
CC   fully defined 123 amino acid sequence given in the specification, which
CC   polypeptide, variant or derivative has at least 20% of the activity of
CC   native HK-D3 in inhibiting angiogenesis, endothelial cell proliferation
CC   or endothelial tube formation in an in vitro or in vivo bioassay. (I) is
CC   useful for inhibiting cell migration, cell invasion, cell proliferation
CC   or angiogenesis, or for inducing apoptosis, which involves contacting
CC   cells associated with undesired cell migration, invasion, proliferation
CC   or angiogenesis with (I). (I) is useful for treating a subject having a disease or
CC   condition associated with undesired cell migration, invasion,
CC   proliferation or angiogenesis. (VI) or (VII) is useful for providing to a
CC   cell, tissue or organ an angiogenesis-inhibitory amount of HK-D3, HK-D3v
CC   or its variant. (I) is useful for treating cancer. This sequence
CC   corresponds to the variant HK-D3v(GS) protein which has an extra 2 amino
CC   acids (Gly-Ser) at the N-terminus of the HK-D3 protein (ADY71956).
XX
SQ   Sequence 125 AA;

Qy   Best Match
     Query Match          100.0%;  Score 670;  DB 9;  Length 125;
     Best Local Similarity 100.0%;  Pred. No. 3.3e-67;
     Matches  125;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ 60

Qy   61 VVAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120

Qy  121 QPLGM 125
         |||||
Db  121 QPLGM 125
```

RESULT 3

```
ID   AAY95426
AC   AAY95426 standard; peptide; 123 AA.
XX
AC   AAY95426;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human high mol.wt. kininogen domain 3.
XX
KW   human; D3 peptide.
KW   rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic therapy;
KW   endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW   Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
XX
OS   Homo sapiens.
XX
PN   WO200035407-A2.
XX
PD   22-JUN-2000.
XX
PF   02-DEC-1999; 99WO-US028465.
XX
PR   16-DEC-1998; 98US-0112427P.
XX
PA   (UTEM ) UNIV TEMPLE.
PA   (MCCR/) MCCRAE R K.
XX
PI   McCrae RK;
XX
DR   WPI; 2000-442247/38.
XX
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```
PT   Composition for inhibiting angiogenesis and endothelial cell
PT   proliferation, inducing endothelial cell apoptosis and treating cancer,
PT   rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3
PT   analog.
XX
PS   Disclosure; Page 4; 44pp; English.
XX
CC   The present sequence is that of domain 3 of human high mol.wt. kininogen
CC   (HK). The invention provides peptides (see AAY95405-24) that are
CC   analogues of certain sites in the HK domain 3, specifically Asn275-
CC   Lys282, Cys246-Cys249, Leu331-Tyr338 and Tyr299-Ser314. The peptides, in
CC   which native Cys residues may be replaced by Ala residues, inhibit
CC   endothelial cell proliferation and may also induce endothelial cell
CC   apoptosis. Compositions including the peptides are used in claimed
CC   methods for inhibiting angiogenesis, inhibiting endothelial cell
CC   proliferation, and inducing endothelial cell apoptosis. Cancer,
CC   rheumatoid arthritis, and ocular disorders characterized by undesired
CC   vascularization of the retina are treated
XX
SQ   Sequence 123 AA;

Query Match             98.5%;  Score 660;  DB 3;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 4.4e-66;
Matches 123;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60

Qy      63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120

Qy     123 LGM 125
           |||
Db     121 LGM 123


RESULT 4
ADM16602
ID   ADM16602 standard; protein; 123 AA.
XX
AC   ADM16602;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Native HK-D3 amino acid sequence, seq id 1.
XX
OS   Homo sapiens.
XX
KW   Cytostatic; nootropic; neuroprotective; antiparkinsonian; inhibitor;
KW   cell migration; cell invasion; cell proliferation; angiogenesis;
KW   apoptosis; tumour growth rate; human kininogen domain 3v; HK-D3;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   amyotrophic lateral sclerosis; ALS.
XX
PN   WO2004024877-A2.
XX
PD   25-MAR-2004.
XX
PF   15-SEP-2003; 2003WO-US028881.
XX
PR   13-SEP-2002; 2002US-0410279P.
XX
PA   (ATTE-) ATTENUON LLC.
XX
PI   Donate F, Mazar A;
XX
DR   WPI; 2004-270022/25.
DR   N-PSDB; ADM16605.
XX
PT   Novel isolated anti-angiogenic polypeptide comprising sequence of human
PT   kininogen domain 3v (HK-D3v) or variant of native HK-D3, useful for
```

```
PT   inhibiting angiogenesis, endothelial cell proliferation or endothelial
PT   tube formation.
XX
PS   Claim 1; SEQ ID NO 1; 79pp; English.
XX
CC   The invention relates to an isolated anti-angiogenic polypeptide (I)
CC   comprising the sequence of human kininogen domain 3v (HK-D3v) (fully
CC   defined sequence (S1) of 127 amino acids as given in specification) or
CC   variant or derivative of native HK-D3 (fully defined sequence (S2) of 123
CC   amino acids as given in specification), and has at least 20% of activity
CC   of native HK-D3 in inhibiting angiogenesis, endothelial cell
CC   proliferation or endothelial tube formation. Also disclosed is a
CC   diagnostically or therapeutically labelled anti-angiogenic polypeptide
CC   (II) comprising (I) labelled with a diagnostic or therapeutic label,
CC   a diagnostic HK-D3-related composition (III) comprising (II) labelled
CC   with a detectable label and a carrier. Further disclosed is an affinity
CC   ligand (IX) useful for binding to or isolating an HK-D3-binding molecule
CC   or cells expressing the binding molecule, comprising (I) immobilized to a
CC   solid support or carrier, (I) or (II) are useful for inhibiting cell
CC   migration, cell invasion, cell proliferation or angiogenesis, or for
CC   inducing apoptosis which involves contacting cells associated with
CC   undesired cell migration, invasion, proliferation or angiogenesis with
CC   (I). (I) is useful for treating neurodegenerative diseases e.g.,
CC   Alzheimer's disease, Parkinson's disease or amyotrophic lateral sclerosis
CC   (ALS). The current sequence represents the native HK-D3 amino acid
CC   sequence.
XX
SQ   Sequence 123 AA;

Query Match             98.5%;  Score 660;  DB 8;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 4.4e-66;
Matches 123;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60

Qy      63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120

Qy     123 LGM 125
           |||
Db     121 LGM 123


RESULT 5
ADY71956
ID   ADY71956 standard; protein; 123 AA.
XX
AC   ADY71956;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Native human kininogen domain 3 protein.
XX
OS   Homo sapiens.
XX
KW   protein engineering; kininogen; antiangiogenic; apoptosis; angiogenesis;
KW   cancer; cytostatic.
XX
PN   US2005058599-A1.
XX
PD   17-MAR-2005.
XX
PF   15-SEP-2003; 2003US-00661784.
XX
PR   15-SEP-2003; 2003US-00661784.
XX
PA   (DONA/) DONATE F.
PA   (MAZA/) MAZAR A P.
XX
PI   Donate F, Mazar AP;
```

Left column

XX
DR
XX
PT Novel human kininogen domain 3 variant inhibiting angiogenesis,
PT endothelial cell proliferation or endothelial tube formation, useful for
PT treating disease associated with undesired cell migration, invasion,
PT proliferation or angiogenesis.
XX
PS
XX
PA

WPI; 2005-213544/22.

Claim 1; SEQ ID NO 1; 35pp; English.

The invention relates to an isolated anti-antiangiogenic polypeptide (I)
having the sequence of human kininogen domain 3 variant (HK-D3v) having a
fully defined 127 amino acid sequence given in the specification, or its
variant or derivative, a variant or derivative of native HK-D3 having a
fully defined 123 amino acid sequence given in the specification, which
variant or derivative has at least 20% of the activity of
polypeptide, variant or derivative of the native HK-D3
native HK-D3 in inhibiting angiogenesis, endothelial cell proliferation
or endothelial tube formation in an in vitro or in vivo bioassay. (I) is
useful for inhibiting cell migration, invasion, cell proliferation
or angiogenesis, or for inducing apoptosis, which involves contacting
cells associated with undesired cell migration, invasion, proliferation
or angiogenesis with (I) or a therapeutically labeled (I). A composition
comprising (I) is useful for treating a subject having a disease or
condition associated with undesired cell migration, invasion,
proliferation or angiogenesis. (VI) or (VII) is useful for providing to a
cell, tissue or organ an angiogenesis-inhibitory amount of HK-D3, HK-D3v
or its variant. (I) is useful for treating cancer. This sequence
corresponds to the native HK-D3 protein sequence.

Sequence 123 AA;

```
Qy   Best Local Similarity   98.5%;   Score 660; DB 9; Length 123;
     Matches 123;  Conservative  100.0%;  Pred. No. 4.4e-66; Mismatches  0; Indels  0; Gaps  0;

Qy     3  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  60

Qy    63  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120

Qy   123  LGM 125
          |||
Db   121  LGM 123
```

RESULT 6
ID   ADP43683 standard; protein; 268 AA.
XX
AC   ADP43683;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human PMMM-40 protein SEQ ID NO:40.
XX
KW   human; protein modification and maintenance molecule; PMMM;
KW   gastrointestinal; cardiovascular; immunosuppressive; antiinflammatory;
KW   cytostatic; neuroprotective; gynaecological; gene therapy;
KW   gastrointestinal disorder; cardiovascular disorder; autoimmune disorder;
KW   inflammatory disorder; cell proliferative disorder;
KW   developmental disorder; epithelial disorder; neurological disorder;
KW   reproductive disorder.
XX
OS   Homo sapiens.
XX

PN   WO20040530068-A2.
XX
PD   24-JUN-2004.
XX
PP   03-DEC-2003; 2003WO-US038573.

Right column

XX
PR
PR
PR
PR
PR 05-DEC-2002; 2002US-0431639P.
PR 17-DEC-2002; 2002US-0434315P.
PR 24-JAN-2003; 2003US-0442442P.
PR 30-JAN-2003; 2003US-0444141P.
PR 21-FEB-2003; 2003US-0449491P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Becha SD, Hafalla AJA, Swarnakar A, Ramkumar J, Richardson TW;
PI Kable AE, Marquis JP, Khare R, Lee SY, Tran UK, Bhatia UG;
PI Burrill JD, Blake JJ, Ho A, Zheng W, Gao J, Chawla NK, Mason PM;
PI Jin P, Lee S;
XX
PN WPI; 2004-468843/44.
DR N-PSDB; ADP43724.
XX
PT New human protein modification and maintenance molecules and
PT polynucleotides for diagnosing, preventing or treating diseases
PT associated with aberrant protein expression, e.g. cardiovascular or cell
PT proliferative disorders.
XX
PS
XX

Claim 1; SEQ ID NO 40; 268pp; English.

The present sequence represents a human protein modification and
maintenance molecule (PMMM) (II), designated PMMM-40. Also described; (1)
an isolated polynucleotide encoding (I); (2) a recombinant polynucleotide
comprising a promoter sequence operably linked to the polynucleotide in
(1); (3) a cell transformed with the recombinant polynucleotide; (4) a
transgenic organism comprising the recombinant polynucleotide; (5)
methods of producing or purifying (I); (6) an isolated antibody that
specifically binds to (I); (7) detecting the polypeptide, an agonist
in a sample; (8) compositions comprising the target polynucleotide or
compound, an antagonist compound or an antibody, and an excipient; (9)
treating diseases or conditions associated with decreased expression or
overexpression of functional human PMMM; (10) screening for a compound
that is effective as an agonist or antagonist of (I), that specifically
binds to (I), that modulates the activity of (I), or is effective in
altering expression of the target polynucleotide; (11) screening for
potential toxicity of a test compound; (12) a diagnostic test for a
condition or disease associated with the expression of PMMM in a
biological sample; (13) diagnosing a condition or disease associated with
the expression of PMMM in a subject; (14) preparing a polyclonal or
monoclonal antibody with the specificity of the antibody in (6); (15) a
polyclonal or monoclonal antibody produced by the method in (14); (16)
compositions comprising the polyclonal or monoclonal antibody, and a
carrier; (17) generating an expression profile of a sample containing the
polynucleotides; and (18) an array comprising different nucleotide
molecules affixed at distinct physical locations on a solid substrate,
where at least one nucleotide molecule comprises a first oligonucleotide
or polynucleotide sequence specifically hybridisable with at least 30
contiguous nucleotides of the target polynucleotide. PMMM sequences have
cytostatic, neuroprotective, immunosuppressive, antiinflammatory,
gastrointestinal, cardiovascular and gynaecological activities, and can be
used in gene therapy. The composition and methods are useful for
diagnosing, preventing or treating diseases or conditions associated with
aberrant expression of PMMM, such as gastrointestinal, cardiovascular,
neurological or reproductive disorders. They may also be used for
autoimmune/inflammatory, cell proliferative, developmental, epithelial,
assessing the effects of exogenous compounds on the expression of nucleic
acid and amino acid sequences of PMMM. The PMMM or its fragments are also
useful in screening compounds for effectiveness as agonist or antagonist
of the polypeptide, or in altering the expression of the target
polynucleotide and compounds that specifically bind to or modulate the
activity of the polypeptide. The microarray is useful in monitoring or
measuring protein-protein interactions, drug-target interactions, and
gene expression profiles.

Sequence 268 AA;

```
Qy   Query Match     98.5%;   Score 660; DB 8; Length 268;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-65; Mismatches  0; Indels  0; Gaps  0;
     Matches 123;  Conservative
```

```
Qy    3  GKDFVQPPTKICVGCPRDIFTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94  GKDFVQPPTKICVGCPRDIFTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  153

Qy   63  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVVPWEKKIYPTVNCQP  122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  154  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVVPWEKKIYPTVNCQP  213

Qy  123  LGM  125
         |||
Db  214  LGM  216
```

RESULT 7
ABM83721

```
ID   ABM83721 standard; protein; 268 AA.
XX
AC   ABM83721;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3970.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI   Harthehorne TA, Sucholeiki MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42373.
XX
CC   New diagnostic and therapeutic polynucleotides and polypeptides, useful
CC   in diagnosing a condition, disease or disorder associated with human
CC   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
CC   in gene mapping.
```

Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotide (dithp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The dithp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a dithp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly

```
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 268 AA;
XX
CC
```

```
Query Match             98.5%;  Score 660;  DB 8;  Length 268;
Best Local Similarity   100.0%;  Pred. No. 1.3e-65;
Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3  GKDFVQPPTKICVGCPRDIFTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94  GKDFVQPPTKICVGCPRDIFTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  153

Qy   63  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVVPWEKKIYPTVNCQP  122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  154  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVVPWEKKIYPTVNCQP  213

Qy  123  LGM  125
         |||
Db  214  LGM  216
```

RESULT 8
ABP70801

```
ID   ABP70801 standard; protein; 304 AA.
XX
AC   ABP70801;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Human extracellular messenger, EXMES-28.
XX
KW   Human; extracellular messenger; EXMES; cytostatic; antidiabetic;
KW   immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
KW   endocrine disorder; cancer.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003018612-A2.
XX
PD   06-MAR-2003.
XX
PF   22-AUG-2002; 2002WO-US027213.
XX
PR   24-AUG-2001; 2001US-0314881P.
PR   14-DEC-2001; 2001US-0340584P.
PR   18-JAN-2002; 2002US-0350559P.
PR   11-MAR-2002; 2002US-0363432P.
PR   15-MAR-2002; 2002US-0364607P.
PR   05-APR-2002; 2002US-0370761P.
PR   24-JUN-2002; 2002US-0391378P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;
PI   Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;
PI   Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y;
PI   Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
PI   Ramkumar J;
XX
DR   WPI; 2003-278643/27.
DR   N-PSDB; ACC42388.
XX
CC   New human extracellular messenger (EXMES) polypeptide, useful for
CC   preparing a composition for treating a disease associated with decreased
CC   expression or overexpression of functional EXMES e.g. autoimmune
CC   disorders or cancer.
```

Claim 1; Page 207; 224pp; English.

The present invention relates to novel human extracellular messenger
proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences
(ACC42361-ACC42388). The proteins are useful for preparing a composition
for diagnosing or treating a disease or condition associated with

```
CC   decreased expression or overexpression of functional EXMES e.g.
CC   autoimmune/inflammatory disorders, diabetes, endocrine disorders or
CC   cancer
XX
SQ   Sequence 304 AA;
XX

Qy   Query Match    98.5%;  Score 660;  DB 6;  Length 304;
Db   Best Local Similarity   100.0%;  Pred. No. 1.5e-65;
     Matches 123;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  130 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 189

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  190 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 249

Qy  123 LGM 125
         |||
Db  250 LGM 252
```

```
RESULT 9
ID   ABM83720 standard; protein; 304 AA.
XX
AC   ABM83720;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3969.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO200402397 3-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI   Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42372.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   polynucleotide and therapeutic polynucleotide (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
```

```
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 304 AA;
XX

Qy   Query Match    98.5%;  Score 660;  DB 8;  Length 304;
Db   Best Local Similarity   100.0%;  Pred. No. 1.5e-65;
     Matches 123;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  130 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 189

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  190 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 249

Qy  123 LGM 125
         |||
Db  250 LGM 252
```

```
RESULT 10
ID   ABP70799 standard; protein; 322 AA.
XX
AC   ABP70799;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Human extracellular messenger, EXMES-26.
XX
KW   Human; extracellular messenger; EXMES; cytostatic; antidiabetic;
KW   immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
KW   endocrine disorder; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200301861 2-A2.
XX
PD   06-MAR-2003.
XX
PF   22-AUG-2002; 2002WO-US027213.
XX
PR   24-AUG-2001; 2001US-0314811P.
PR   14-DEC-2001; 2001US-0340584P.
PR   18-JAN-2002; 2002US-0350595P.
PR   11-MAR-2002; 2002US-0363432P.
PR   15-MAR-2002; 2002US-0364607P.
PR   05-APR-2002; 2002US-0370761P.
PR   24-JUN-2002; 2002US-0391378P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
PI   Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;
PI   Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;
PI   Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y;
PI   Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
PI   Ramkumar J;
XX
DR   WPI; 2003-278643/27.
DR   N-PSDB; ACC42386.
XX
PT   New human extracellular messenger (EXMES) polypeptide, useful for
PT   preparing a composition for treating a disease associated with decreased
```

PT   expression or overexpression of functional EXMES e.g. autoimmune
PT   disorders or cancer.
XX
PS   Claim 1; Page 205-206; 224pp; English.
XX
CC   The present invention relates to novel human extracellular messenger
CC   proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences
CC   (ACC42361-ACC42388). The proteins are useful for preparing a composition
CC   for diagnosing or treating a disease or condition associated with
CC   decreased expression or overexpression of functional EXMES e.g.
CC   autoimmune/inflammatory disorder, diabetes, endocrine disorders or
CC   cancer
XX
SQ   Sequence 322 AA;
XX

Qy   Query Match   98.5%; Score 660; DB 6; Length 322;
     Best Local Similarity 100.0%; Pred. No. 1.6e-65;
     Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 207

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 267

Qy   123 LGM 125
          |||
Db   268 LGM 270

RESULT 11
ABM83717
ID   ABM83717 standard; protein; 326 AA.
XX
AC   ABM83717;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3966.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
XX
PN   WO200402973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2002; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI   Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Steve LL;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CJ;
XX
DR   WPI; 2004-329568/30.
DR   N-PSDB; ACN42369.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.

XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 326 AA;
XX

Qy   Query Match   98.5%; Score 660; DB 8; Length 326;
     Best Local Similarity 100.0%; Pred. No. 1.7e-65;
     Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   152 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 211

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 271

Qy   123 LGM 125
          |||
Db   272 LGM 274

RESULT 12
ABU92044
ID   ABU92044 standard; protein; 329 AA.
XX
AC   ABU92044;
XX
DT   15-JUL-2003 (first entry)
XX
DE   Human protein modification and maintenance molecule-24 (PMMM-24).
XX
KW   Human; protein modification and maintenance molecule; PMMM; cancer;
KW   cell proliferation disorder; atherosclerosis; neurological disorder;
KW   epilepsy; Huntington's disease; stroke; immune disorder; allergy;
KW   inflammatory disorder; AIDS; developmental disorder; hypothyroidism;
KW   Cushing's syndrome; gastrointestinal disorder; epithelial disorder;
KW   infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
KW   neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary;
KW   antiinflammatory; thyromimetic.
XX
OS   Homo sapiens.
XX
XX
PN   WO200303199-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032850.
XX
PR   12-OCT-2001; 2001US-0329689P.
PR   25-OCT-2001; 2001US-0335703P.
PR   09-NOV-2001; 2001US-0348887P.
PR   28-NOV-2001; 2001US-0334145P.
PR   06-DEC-2001; 2001US-0337451P.
PR   14-DEC-2001; 2001US-0340584P.
XX

(INCY-) INCYTE GENOMICS INC.

```
PA
XX
PI  Rankumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;
PI  Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;
PI  Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue H;
PI  Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;
PI  Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
XX
DR  WPI; 2003-430274/40.
DR  N-PSDB; ACA92439.
XX
PS  Claim 1; Page 264-265; 311pp; English.
XX
PT  The present invention relates to the isolation of human protein
PT  modification and maintenance molecules (PMMM), and the polynucleotide
PT  sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM
PT  -1 to PMMM-40) are disclosed. The sequences of the invention are useful
PT  for diagnosing a condition or disease associated with the expression of
PT  PMMM in a subject, preparing a polyclonal or monoclonal antibody, and
PT  generating an expression profile of a sample containing the
PT  polynucleotides. The diseases or conditions associated with decreased
PT  expression or overexpression of PMMM are cell proliferation disorders
PT  (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,
PT  Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS,
PT  allergies), developmental disorders (e.g. hypothyroidism, Cushing's
PT  syndrome), gastrointestinal or epithelial disorders, and infections. The
PT  PMMM polypeptides or their fragments are useful in screening compounds
PT  for effectiveness as agonists or antagonists of the polypeptides, or in
PT  specifically bind to, or modulate the activity of the polypeptide.
PT  altering the expression of the target polynucleotide and compounds that
CC  New human protein modification and maintenance molecules (PMMM), useful
CC  for diagnosing, treating and preventing diseases or conditions associated
CC  with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
CC  infections.
XX
PN  ABU92021-ABU92060 represent the human PMMM polypeptides of the invention
SQ  Sequence 329 AA;

Qy  Query Match        98.5%; Score 660; DB 6; Length 329;
    Best Local Similarity  100.0%; Pred. No. 1.7e-65;
    Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 214

Qy     63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 274

Qy    123 LGM 125
          |||
Db    275 LGM 277
```

RESULT 13

```
ID  ABM83716
AC  ABM83716;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Human diagnostic and therapeutic pprotein SEQ ID NO:3965.
KW  gene therapy; human diagnostic and therapeutic polynuclectide; dithp.
XX
OS  Homo sapiens.
XX
PN  WO200402973-A2.
XX
PD  25-MAR-2004.
```

```
XX
PF  12-SEP-2003; 2003WO-US028227.
XX
PR  12-SEP-2002; 2002US-0410259P.
PR  12-SEP-2002; 2002US-0410260P.
XX
```

(INCY-) INCYTE CORP.

```
PA
PI  Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI  Harthehorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI  Mooney EM, Delegeane AM, Panesar SR, Banville SC, Reddy TP;
PI  Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI  Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI  Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI  Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI  Patury S, Shi X, Suarez CJ;
XX
DR  WPI; 2004-329368/30.
DR  N-PSDB; ACN42368.
XX
PS  Claim 27; Page; 190pp; English.
XX
PT  The invention relates to novel diagnostic and therapeutic polynucleotides
PT  and therapeutic polynucleotides and polypeptides, useful
PT  in diagnosing a condition, disease or disorder associated with human
PT  molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT  in gene mapping.
XX
CC  New diagnostic and therapeutic polynucleotides and polypeptides, useful
CC  in diagnosing a condition, disease or disorder associated with human
CC  molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
CC  in gene mapping.
CC  The invention relates to novel diagnostic and therapeutic polynucleotides
CC  selected from one of the 2722 sequences defined in the specification. A
CC  polynucleotide of the invention may have a use in gene therapy. The human
CC  diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC  used to diagnose a particular condition, disease or disorder associated
CC  with human molecules, e.g. cell proliferative disorders,
CC  autoimmune/inflammatory disorder, developmental disorder, endocrine
CC  disorder, neurological disorders, gastrointestinal disorders, or
CC  infections caused by virus, bacteria, fungi or parasite. The dithp
CC  molecules may also be used in genetic mapping, in identifying individuals
CC  from minute biological samples, in detecting single nucleotide
CC  polymorphisms, as molecular weight markers, and for somatic or germline
CC  gene therapy. The present sequence represents a dithp protein of the
CC  invention. Note: The sequence data for this patent is not represented in
CC  the printed specification, but was obtained in electronic format directly
CC  from WIPO at www.wipo.int/pct/en/sequences/listing.htm
SQ  Sequence 329 AA;

Qy  Query Match        98.5%; Score 660; DB 8; Length 329;
    Best Local Similarity  100.0%; Pred. No. 1.7e-65;
    Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 214

Qy     63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 274

Qy    123 LGM 125
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Db    275 LGM 277
```

RESULT 14

```
ID  ABP70800
AC  ABP70800;
XX
DT  26-AUG-2003 (first entry)
XX
DE  Human extracellular messenger, EXMES-27.
XX
```

KW   Human; extracellular messenger; EXMES; cytostatic; antidiabetic;
KW   immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
KW   endocrine disorder; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003018612-A2.
XX
PD   06-MAR-2003.
XX
PF   22-AUG-2002; 2002WO-US027213.
XX
PR   24-AUG-2001; 2001US-0314881P.
PR   14-DEC-2001; 2001US-0340584P.
PR   18-JAN-2002; 2002US-0350595P.
PR   11-MAR-2002; 2002US-0363432P.
PR   15-MAR-2002; 2002US-0364607P.
PR   05-APR-2002; 2002US-0370761P.
PR   24-JUN-2002; 2002US-0391378P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;
PI   Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;
PI   Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y;
PI   Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
PI   Ramkumar J;
XX
DR   WPI; 2003-278643/27.
DR   N-PSDB; ACC42387.
XX
PT   New human extracellular messenger (EXMES) polypeptide, useful for
PT   preparing a composition for treating a disease associated with decreased
PT   expression or overexpression of functional EXMES e.g. autoimmune
PT   disorders or cancer.
XX
PS   Claim 1; Page 206; 224pp; English.
XX
CC   The present invention relates to novel human extracellular messenger
CC   proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences
CC   (ACC42361-ACC42388). The proteins are useful for preparing a composition
CC   for diagnosing or treating a disease or condition associated with
CC   decreased expression or overexpression of functional EXMES e.g.
CC   autoimmune/inflammatory disorders, diabetes, endocrine disorders or
CC   cancer.
XX
SQ   Sequence 358 AA;

Query Match   98.5%; Score 660; DB 6; Length 358;
Best Local Similarity   100.0%; Pred. No. 1.9e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEBTLTHTITIKLNAENNATFYFKIDNVKKARVQVV 62
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Db 184 GKDFVQPPTKICVGCPRDIPTNSPELEBTLTHTITIKLNAENNATFYFKIDNVKKARVQVV 243

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 244 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 303

Qy 123 LGM 125
         |||
Db 304 LGM 306

RESULT 15
AEB32339

ID   AEB32339 standard; protein; 362 AA.
XX
AC   AEB32339;
XX
DT   08-SEP-2005 (first entry)
XX
DE   Human protein #41.
XX
KW   SNP detection; diagnosis; non-insulin dependent diabetes; obesity;
KW   antidiabetic; anorectic; endocrine disease; gastrointestinal disease;
KW   metabolic disorder; nutritional disorder.
XX
OS   Homo sapiens.
XX
PN   US2005147987-A1.
XX
PD   07-JUL-2005.
XX
PF   19-JUL-2004; 2004US-00893315.
XX
PR   08-SEP-2000; 2000US-0231397P.
PR   10-SEP-2001; 2001US-00948947.
XX
PA   (APPL-) APPLERA CORP NY.
XX
PI   Venter JC, Zhang JN, Liu X, Rowe W, Cravchik A, Kalush F;
PI   Naik A, Subramanian G, Woodage T;
XX
DR   WPI; 2005-511776/52.
DR   N-PSDB; AEB32278.
XX
PT   New detection reagent capable of detecting 1, 100, 500, 1000 or 5000 or
PT   more single nucleic acid polymorphisms, useful in identifying an
PT   individual having or at risk of developing type II diabetes or obesity.
XX
PS   Disclosure; SEQ ID NO 102; 31pp; English.
XX
CC   The invention relates to a detection reagent capable of detecting one or
CC   more single nucleic acid polymorphisms. The invention also relates to
CC   determining whether a trait is linked to one of the human chromosomes or
CC   its sub-region, a computer readable medium having stored in it the SNP
CC   relational information given in the specification, an isolated nucleic
CC   acid molecule for detecting at least one SNP given in the specification
CC   comprising at least about 12 contiguous nucleotides, genotyping at least
CC   one SNP position given in the specification in a sample, identifying an
CC   individual having or at risk of developing a disorder and a kit
CC   comprising at least one container containing the detection reagent.
CC   Determining whether a trait is linked to one of the human chromosomes or
CC   its sub-region comprises determining whether the trait is linked to one
CC   or more SNPs using the detection reagents. Genotyping at least one SNP
CC   position given in the specification comprises contacting the
CC   sample with a detection reagent that differentiates between alternative
CC   alleles at at least one SNP position given in the specification, and
CC   determining which allele is present at the at least one SNP position.
CC   Identifying an individual having or at risk of developing a disorder
CC   comprises genotyping at least one SNP given in the specification in a
CC   nucleic acid sample from the individual. The disorder is type II diabetes
CC   (non-insulin dependent diabetes) or obesity. The detection reagent is
CC   useful in identifying an individual having or at risk of developing a
CC   disorder, particularly type II diabetes or obesity. This sequence
CC   represents a human protein used in the scope of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 362 AA;

Query Match   98.5%; Score 660; DB 9; Length 362;
Best Local Similarity   100.0%; Pred. No. 1.9e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEBTLTHTITIKLNAENNATFYFKIDNVKKARVQVV 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188 GKDFVQPPTKICVGCPRDIPTNSPELEBTLTHTITIKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 307

```
Qy    123 LGM 125
          |||
Db    308 LGM 310
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Search completed: February 8, 2006, 03:12:51
Job time : 202 secs

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OM protein - protein search, using sw model

                      Copyright (c) 1993 - 2006 Biocceleration Ltd.
                      GenCore version 5.1.7

Run on:    February 8, 2006, 03:17:23 ; Search time 48 Seconds
                                         (without alignments)
                                         215.301 Million cell updates/sec

Title:            US-10-661-784-2
Perfect score:    670
Sequence:         1 GSGKDFVQPPTKICVGCPRD..........YVVPWEKKIYPTVNCQPLGM 125
Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5
Searched:         572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:   572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued patents AA:*
              1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
              2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
              3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
              4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
              6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	660	98.5	123	2	US-09-461-061-18	Sequence 18, Appl
2	660	98.5	362	2	US-09-949-002-476	Sequence 476, App
3	660	98.5	362	2	US-09-949-002-480	Sequence 480, App
4	660	98.5	427	2	US-09-919-039-29	Sequence 29, Appl
5	660	98.5	579	2	US-09-949-002-475	Sequence 475, App
6	660	89.5	579	2	US-09-949-002-481	Sequence 481, App
7	600	89.6	117	2	US-08-193-114B-1	Sequence 1, Appli
8	594	88.5	117	4	PCT-US92-06809-1	Sequence 1, Appli
9	169	25.2	178	1	US-08-791-522-1	Sequence 1, Appl
10	169	24.8	178	1	US-08-314-777-1	Sequence 1, Appl
11	166	24.8	32	2	US-09-461-061-17	Sequence 17, Appl
12	165.5	24.7	145	1	US-08-832-535-2	Sequence 2, Appl
13	165.5	24.7	145	1	US-08-019-485-3	Sequence 3, Appl
14	165.5	24.7	145	2	US-09-019-485-2	Sequence 2, Appl
15	165.5	24.7	145	2	US-09-431-480-9	Sequence 9, Appl
16	165.5	24.7	145	2	US-09-617-302-9	Sequence 9, Appl
17	165.5	24.7	145	2	US-09-528-436B-2	Sequence 2, Appl
18	161	24.0	32	2	US-09-461-061-4	Sequence 4, Appl
19	155	23.1	27	2	US-08-676-242-11	Sequence 11, Appl
20	153	22.8	27	2	US-09-461-061-8	Sequence 8, Appl
21	145	21.6	64	2	US-08-676-242-22	Sequence 22, Appl
22	145	21.6	64	2	US-09-402-732-11	Sequence 11, Appl
23	138.5	20.7	121	2	US-09-775-932-14	Sequence 14, Appl
24	138.5	20.7	128	2	US-09-775-932-12	Sequence 12, Appl
25	138.5	20.7	149	1	US-08-461-030C-2	Sequence 2, Appli
26	138.5	20.7	149	2	US-08-744-138-2	Sequence 2, Appli
27	138.5	20.7	149	2	US-09-431-480-8	Sequence 8, Appli
28	138.5	20.7	149	2	US-09-431-480-10	Sequence 10, Appli
29	138.5	20.7	149	2	US-09-617-302-8	Sequence 8, Appli
30	138.5	20.7	149	2	US-09-617-302-10	Sequence 10, Appli
31	138.5	20.7	149	2	US-09-241-376-2	Sequence 2, Appli
32	138.5	20.7	149	2	US-08-940-497-2	Sequence 2, Appli
33	136	20.3	112	2	US-08-849-303-16	Sequence 16, Appl
34	135	20.1	118	2	US-09-775-932-24	Sequence 24, Appl
35	134	20.0	148	4	PCT-US95-07135-2	Sequence 2, Appl
36	132	19.7	26	2	US-08-676-242-15	Sequence 15, Appl
37	130	19.4	127	2	US-09-886-319A-46	Sequence 46, Appl
38	129.5	19.3	140	2	US-09-886-319A-48	Sequence 48, Appl
39	129.5	19.3	382	2	US-09-886-303-19	Sequence 19, Appl
40	129.5	19.3	314	2	US-09-599-360B-93	Sequence 93, Appl
41	129.5	19.2	146	6	5432264	Patent No. 5432264
42	128.5	19.2	146	1	US-08-849-303-26	Sequence 26, Appl
43	128	19.1	111	2	US-09-775-932-2	Sequence 2, Appli
44	127.5	19.1	120	2	US-09-431-480-5	Sequence 5, Appli
45	127.5	19.0	140	2	US-09-431-480-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-461-061-18
; Sequence 18, Application US/09461061
; Patent No. 6869931
; GENERAL INFORMATION:
; APPLICANT: McCrae, Keith R.
; TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
; TITLE OF INVENTION: Kininogen Domain 3 Peptide Analogs
; FILE REFERENCE: 6056-260 US
; CURRENT APPLICATION NUMBER: US/09/461,061
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,427
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human HK
; OTHER INFORMATION: domain 3
US-09-461-061-18

  Query Match             98.5%;  Score 660;  DB 2;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1e-65;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
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Db    1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVPWEKKIYPTVNCQP 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGKKYFIDFVARETTCSKESNEELTBSCETKKLGQSLDCNAEVVVPWEKKIYPTVNCQP 120

Qy  123 LGM 125
          |||
Db  121 LGM 123

RESULT 2
US-09-949-002-476
; Sequence 476, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
```

; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 476
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-476

Query Match   98.5%; Score 660; DB 2; Length 362;
Best Local Similarity   100.0%; Pred. No. 4.3e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 307

Qy   123 LGM 125
           |||
Db   308 LGM 310

RESULT 3
US-09-949-002-480
; Sequence 480, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
;* APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 480
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-480

Query Match   98.5%; Score 660; DB 2; Length 362;
Best Local Similarity   100.0%; Pred. No. 4.3e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 307

Qy   123 LGM 125
           |||
Db   308 LGM 310

RESULT 4
US-09-919-039-29
; Sequence 29, Application US/0991903P
; Patent No. 6727066

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
;
; SEQ ID NO 29
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 167507CD1
US-09-919-039-29

Query Match   98.5%; Score 660; DB 2; Length 427;
Best Local Similarity   100.0%; Pred. No. 5.3e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 372

Qy   123 LGM 125
           |||
Db   373 LGM 375

RESULT 5
US-09-949-002-475
; Sequence 475, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 475
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-475

Query Match   98.5%; Score 660; DB 2; Length 579;
Best Local Similarity   100.0%; Pred. No. 8e-65;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 122
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Db   248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP 307

Qy   123 LGM 125
           |||
Db   308 LGM 310

RESULT 6
US-09-949-002-481
; Sequence 481, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-481

Query Match   98.5%; Score 660; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 8e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFYFKIDNVKKARVQVV 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKSNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 248 AGKKYFIDFVARETTCSKSNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 307

Qy 123 LGM 125
         |||
Db 308 LGM 310

RESULT 7
US-08-193-114B-1
; Sequence 1, Application US/08193114B
; Patent No. 5472945
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Jiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
; TITLE OF INVENTION: with Kininogen Fragment
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna &
; ADDRESSEE: Monaco, P.C.
; STREET: 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,114B
; FILING DATE: 9 February 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 514
; APPLICATION NUMBER: Serial No. 5472945 07/744,545
; FILING DATE: 13 August 1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-137 CII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-5549
; TELEFAX: No. 5472945e.
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: peptide
; TOPOLOGY: linear
US-08-193-114B-1

Query Match   89.6%; Score 600; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.5e-59;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   14 CVGCPRDIPTNSPELEETLTHTITKLNAENNATYFYFKIDNVKKARVQVVAGKKYFIDFVA 73
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CVGCPRDIPTNSPELEETLTHTITKLNAENNATYFYFKIDNVKKARVQVVAGKKYFIDFVA 60

Qy   74 RETTCSKSNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQPLGM 125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RETTCSKSNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQPLGM 112

RESULT 8
PCT-US92-06809-1
; Sequence 1, Application PC/TUS9206809
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Jiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of the
; ADDRESSEE: Commonwealth System of Higher Education
; STREET: 406 University Services
; STREET: Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06809
; FILING DATE: 19910813
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Application
; APPLICATION NUMBER: Serial No. 744,545
; FILING DATE: 13 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US92-06809-1

RESULT 9
US-08-791-522-1
Sequence 1, Application US/08791522
Patent No. 5935817
GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/791,522
;   FILING DATE: Filed Herewith
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0193 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 178 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   CLONE: 30443
US-08-791-522-1

  Query Match   88.7%; Score 594; DB 4; Length 117;
  Best Local Similarity   98.2%; Pred. No. 2.1e-58;
  Matches 110; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   14 CVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVA 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVA 60

Qy   74 RETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM 125
              |||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   61 RETTCSKESNEELTESCETKKLGESLDCNAEVYVVPWEKKIYPTVNCEPLGM 112

RESULT 10
US-09-314-777-1
Sequence 1, Application US/09314777
Patent No. 6110686
GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
; PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/314,777
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/791,522
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0193 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 178 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   CLONE: 30443
US-09-314-777-1

  Query Match   25.2%; Score 169; DB 2; Length 178;
  Best Local Similarity   32.5%; Pred. No. 7.2e-11;
  Matches   39; Conservative   22; Mismatches   49; Indels   10; Gaps   4;

Qy   11 TKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
              ::: |::|:|:||:: :::|:|||||
Db   54 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 113

Qy   71 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVN--CQPLGM 125
              |||| |||||||||:|:|| ||: |:||:|| ||:
Db   114 VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPW----VPALRGACSPLSL 168

RESULT 11
US-09-461-061-17
Sequence 17, Application US/09461061
Patent No. 6869931
GENERAL INFORMATION:
; APPLICANT: McCrae, Keith R.
; TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
; TITLE OF INVENTION: Kininogen Domain 3 Peptide Analogs
; FILE REFERENCE: 6056-260 US
; CURRENT APPLICATION NUMBER: US/09/461,061
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,427
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 21

  Query Match   25.2%; Score 169; DB 1; Length 178;
  Best Local Similarity   32.5%; Pred. No. 7.2e-11;
  Matches   39; Conservative   22; Mismatches   49; Indels   10; Gaps   4;

Qy   11 TKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
              ::: |::|:|:||:: :::|:|||||
Db   54 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 113

Qy   71 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVN--CQPLGM 125
              |||| |||||||||:|:|| ||: |:||:|| ||:
Db   114 VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPW----VPALRGACSPLSL 168

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; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 17
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; OTHER INFORMATION: human HK domain 3 fragment
US-09-461-061-17

Qy     87 TESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
          ||||||||||||||| ||||||||||||||||
Db      1 TESCETKKLGQSLDANAEVYVVPWEKKIYPTV 32

RESULT 12
US-08-832-535-2
; Sequence 2, Application US/08832535
; Patent No. 5919658
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: LI, HAODONG
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L
; TITLE OF INVENTION: HUMAN CYSTATIN F
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,535
; FILING DATE: 03-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KIMBALL, PAUL C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF265
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-832-535-2

Query Match        24.7%;    Score 165.5;   DB 1;   Length 145;
Best Local Similarity    32.5%;   Pred. No. 1.3e-10;
Matches   37;   Conservative   22;   Mismatches   50;   Indels   5;   Gaps   3;

Qy  11 TKICVGCPRDIPTNSPELEETLTHITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
       ||:| |:|:|| |:|:|:|:|||||| ::||:.|||::|:|: :|:||:|:: :|||:
Db  32 SRVKPGPPKTIKTNDPGVLQOAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 91

Qy  71 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC 120
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Db  92 VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC 144
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RESULT 13
US-09-019-485-2
; Sequence 2, Application US/09019485
; Patent No. 6066617
; GENERAL INFORMATION:
; APPLICANT: Li, Haodong
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Cystatin F
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,485
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H.
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PF265P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3013098439
; TELEFAX: 3013098504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-019-485-2

Query Match        24.7%;    Score 165.5;   DB 2;   Length 145;
Best Local Similarity    32.5%;   Pred. No. 1.3e-10;
Matches   37;   Conservative   22;   Mismatches   50;   Indels   5;   Gaps   3;

Qy  11 TKICVGCPRDIPTNSPELEETLTHITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
       ||:| |:|:|| |:|:|:|:|||||| ::||:.|||::|:|: :|:||:|:: :|||:
Db  32 SRVKPGPPKTIKTNDPGVLQOAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 91

Qy  71 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC 120
       ||||| ||:| :|||| ||:|   :|||||||||||||||||||||| :|||||
Db  92 VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC 144

RESULT 14
US-09-019-485-3
; Sequence 3, Application US/09019485
; Patent No. 6066617
; GENERAL INFORMATION:
; APPLICANT: Li, Haodong
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Cystatin F
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
```

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;           ZIP: 20850
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: Patentin Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/019,485
;       FILING DATE:
;    CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Benson, Robert H.
;       REGISTRATION NUMBER: 30,446
;       REFERENCE/DOCKET NUMBER: PF265P1
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 301309504
;       TELEFAX: 301309439
; INFORMATION FOR SEQ ID NO: 3:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 145 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-09-019-485-3 .

Query Match            24.7%;   Score 165.5; DB 2;  Length 145;
Best Local Similarity   32.5%;   Pred. No. 1.3e-10;
    Matches  37;   Conservative  22;   Mismatches  50;   Indels  5;   Gaps  3;

Qy       11  TKICVGCPRDIPTNSPELEETLTHTTTKLNAENNATFYFKIDNVKKARVQVVAGKKYFID   70
                 |||     ||| :|  |||:||| :: |||: :: |||||::|||:|: ||:
Db       32  SRVKPGPPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE   91

Qy  •    71  FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC   120
                 ||||     |:  ||| | :   :|||:| || :|: |:|||| |  :|:||
Db       92  VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC  144


RESULT 15
US-09-431-480-9
; Sequence 9, Application US/09431480
; Patent No. 6235708
;    GENERAL INFORMATION:
;       APPLICANT: Holloway, James L.
;       APPLICANT: Feldhaus, Andrew
;       TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
;       FILE REFERENCE: 98-72
;       CURRENT APPLICATION NUMBER: US/09/431,480
;       CURRENT FILING DATE: 1999-11-01
;       EARLIER APPLICATION NUMBER: 60/109,217
;       EARLIER FILING DATE: 1998-11-20
;       EARLIER APPLICATION NUMBER: 60/156,382
;       EARLIER FILING DATE: 1999-09-28
;       NUMBER OF SEQ ID NOS: 22
;    SEQ ID NO 9
;       LENGTH: 145
;       TYPE: PRT
;       ORGANISM: Homo sapiens
US-09-431-480-9

Query Match            24.7%;   Score 165.5; DB 2;  Length 145;
Best Local Similarity   32.5%;   Pred. No. 1.3e-10;
    Matches  37;   Conservative  22;   Mismatches  50;   Indels  5;   Gaps  3;

Qy       11  TKICVGCPRDIPTNSPELEETLTHTTTKLNAENNATFYFKIDNVKKARVQVVAGKKYFID   70
                 |||     ||| :|  |||:||| :: |||: :: |||||::|||:|: ||:
Db       32  SRVKPGPPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE   91

Qy       71  FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC   120
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Db       92  VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC  144
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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:18:07 ; Search time 179 Seconds
(without alignments)
291.780 Million cell updates/sec

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GenCore version 5.1.7

Title: US-10-661-784-2
Perfect score: 670
Sequence: 1 GSGKDFVQPPTKICVGCPRD...........YVVPWEKKIYPTVNCQPLGM 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670	100.0	125	5	US-10-661-784-2	Sequence 2, Appli
2	660	98.5	123	5	US-10-661-784-1	Sequence 1, Appli
3	660	98.5	362	5	US-10-893-315-102	Sequence 104, App
4	660	98.5	362	5	US-10-893-315-104	Sequence 102, App
5	660	98.5	390	4	US-10-162-335-82	Sequence 82, Appl
6	660	98.5	390	5	US-10-637-313-32	Sequence 32, Appl
7	660	98.5	398	4	US-10-162-335-70	Sequence 70, Appl
8	660	98.5	398	3	US-10-637-313-20	Sequence 20, Appl
9	660	98.5	427	3	US-10-919-039-29	Sequence 29, Appl
10	660	98.5	427	5	US-10-637-313-24	Sequence 24, Appl
11	660	98.5	427	5	US-10-741-600-1179	Sequence 1179, Ap
12	660	98.5	427	5	US-10-741-600-1181	Sequence 1181, Ap
13	660	98.5	579	5	US-10-893-315-101	Sequence 101, App
14	660	98.5	579	4	US-10-893-315-105	Sequence 105, App
15	660	98.5	615	4	US-10-162-335-72	Sequence 72, Appl
16	660	98.5	615	5	US-10-637-313-22	Sequence 22, Appl
17	660	98.5	616	5	US-10-637-313-14	Sequence 14, Appl
18	660	98.5	621	5	US-10-637-313-16	Sequence 16, Appl
19	660	98.5	621	5	US-10-637-313-44	Sequence 44, Appl
20	660	98.5	622	5	US-10-637-313-18	Sequence 18, Appl
21	660	98.5	626	5	US-10-507-734-25	Sequence 25, Appl
22	660	98.5	628	5	US-10-637-313-22	Sequence 22, Appl
23	660	98.5	644	4	US-10-162-335-84	Sequence 84, Appl
24	660	98.5	644	4	US-10-162-335-74	Sequence 74, Appl
25	660	98.5	644	5	US-10-637-313-2	Sequence 2, Appli
26	660	98.5	644	5	US-10-637-313-6	Sequence 6, Appli
27	660	98.5	644	5	US-10-637-313-52	Sequence 52, Appl
28	660	98.5	644	5	US-10-637-313-54	Sequence 54, Appl
29	660	98.5	644	5	US-10-637-313-56	Sequence 56, Appl
30	660	98.5	644	5	US-10-637-313-58	Sequence 58, Appl
31	660	98.5	644	5	US-10-637-313-60	Sequence 60, Appl
32	660	98.5	644	5	US-10-637-313-62	Sequence 62, Appl
33	660	98.5	644	5	US-10-637-313-64	Sequence 64, Appl
34	660	98.5	644	5	US-10-637-313-76	Sequence 76, Appl
35	660	98.5	644	5	US-10-741-600-1180	Sequence 1180, A
36	660	98.5	644	5	US-10-450-763-51460	Sequence 51460, A
37	656	97.9	644	5	US-10-637-313-66	Sequence 66, Appl
38	653	97.5	644	5	US-10-637-313-68	Sequence 68, Appl
39	653	97.5	644	5	US-10-637-313-70	Sequence 70, Appl
40	653	97.5	644	5	US-10-637-313-72	Sequence 72, Appl
41	648	96.7	644	5	US-10-637-313-74	Sequence 74, Appl
42	628	93.7	127	5	US-10-661-784-3	Sequence 3, Appli
43	589.5	88.0	435	5	US-10-450-763-51464	Sequence 51464, A
44	554	82.7	357	5	US-10-637-313-10	Sequence 10, Appl
45	554	82.7	357	5	US-10-637-313-46	Sequence 46, Appl

ALIGNMENTS

US-10-661-784-2

RESULT 1
US-10-661-784-2
; Sequence 2, Application US/10661784
; Publication No. US2005005859A1
; GENERAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: MAZAR, Andrew
; TITLE OF INVENTION: Human Kininogen D3 Domain Polypeptide as an Anti-Angiogenic and
; FILE REFERENCE: 38342-193024
; CURRENT APPLICATION NUMBER: US/10/661,784
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/401,279
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-784-2

Query Match 100.0%; Score 670; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e-63;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQ 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GSGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQ 60

Qy 61 VVAGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 VVAGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNC 120

Qy 121 QPLGM 125
        |||||
Db 121 QPLGM 125

RESULT 2
US-10-661-784-1
; Sequence 1, Application US/10661784
; Publication No. US2005005859A1
; GENERAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: MAZAR, Andrew
; TITLE OF INVENTION: Human Kininogen D3 Domain Polypeptide as an Anti-Tumor Agent
; TITLE OF INVENTION: Anti-Tumor Agent
; FILE REFERENCE: 38342-193024
; CURRENT APPLICATION NUMBER: US/10/661,784

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; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/401,279
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 1
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-661-784-1

Query Match             98.5%;  Score 660;  DB 5;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 7.2e-62;
Matches  123;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120

Qy  123 LGM 125
          |||
Db  121 LGM 123


RESULT 3
US-10-893-315-102
; Sequence 102, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 102
;   LENGTH: 362
;   TYPE: PRT
;   ORGANISM: Human
US-10-893-315-102

Query Match             98.5%;  Score 660;  DB 5;  Length 362;
Best Local Similarity   100.0%;  Pred. No. 2.9e-61;
Matches  123;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  188 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 307

Qy  123 LGM 125
          |||
Db  308 LGM 310


RESULT 4
US-10-893-315-104
; Sequence 104, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 104
;   LENGTH: 362
;   TYPE: PRT
;   ORGANISM: Human
US-10-893-315-104

Query Match             98.5%;  Score 660;  DB 5;  Length 362;
Best Local Similarity   100.0%;  Pred. No. 2.9e-61;
Matches  123;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  188 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 307

Qy  123 LGM 125
          |||
Db  308 LGM 310


RESULT 5
US-10-162-335-82
; Sequence 82, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalt, Tord
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Pasturajan, Meera
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
; FILE REFERENCE: 21402-377 B
; CURRENT APPLICATION NUMBER: US/10/162,335
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
```

; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 82
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-82

Query Match   98.5%;   Score 660; DB 4; Length 390;
Best Local Similarity   100.0%;   Pred. No. 3.1e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 275

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 335

Qy   123 LGM 125
            |||
Db   336 LGM 338

RESULT 6
US-10-637-313-32
; Sequence 32, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Rameah Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khramtsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 32
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-32

Query Match   98.5%;   Score 660; DB 5; Length 390;
Best Local Similarity   100.0%;   Pred. No. 3.1e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 275

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVVPWEKKIYPTVNCQP 335

Qy   123 LGM 125
            |||
Db   336 LGM 338

RESULT 7
US-10-162-335-70
; Sequence 70, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalt, Tord
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
; FILE REFERENCE: 21402-377 B
; CURRENT APPLICATION NUMBER: US/10/162,335
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06

US-10-162-335-70
;   ORGANISM: Homo sapiens
;   TYPE: PRT
;   LENGTH: 398
SEQ ID NO 70
;   NUMBER OF SEQ ID NOS: 201
Remaining Prior Application data removed - See File Wrapper or PALM.
;   PRIOR FILING DATE: 2001-06-26
;   PRIOR APPLICATION NUMBER: 60/300,883
;   PRIOR FILING DATE: 2001-06-21
;   PRIOR APPLICATION NUMBER: 60/299,949
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/298,556
;   PRIOR FILING DATE: 2001-06-14
;   PRIOR APPLICATION NUMBER: 60/298,285
;   PRIOR FILING DATE: 2001-06-12
;   PRIOR APPLICATION NUMBER: 60/297,567
;   PRIOR FILING DATE: 2001-06-11
;   PRIOR APPLICATION NUMBER: 60/297,414
;   PRIOR FILING DATE: 2001-06-06
;   PRIOR APPLICATION NUMBER: 60/296,418
;   PRIOR FILING DATE: 2001-06-06

```
Query Match       98.5%;   Score 660;   DB 4;   Length 398;
Best Local Similarity    100.0%;   Pred. No. 3.2e-61;
Matches   123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 283

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 343

Qy        123 LGM 125
              |||
Db        344 LGM 346
```

RESULT 8
US-10-637-313-20
Sequence 20, Application US/10637313
Publication No. US20040229779A1
GENERAL INFORMATION:
;   APPLICANT: Ramesh Kekuda
;   APPLICANT: Uriel Malyankar
;   APPLICANT: Li Li
;   APPLICANT: David Anderson
;   APPLICANT: Sasha Guo
;   APPLICANT: Mei Zhong
;   APPLICANT: Muralidhara Padigaru
;   APPLICANT: Stacie Casman
;   APPLICANT: Ferenc Boldog
;   APPLICANT: Charles Miller
;   APPLICANT: Nikolai Khramtsov
;   APPLICANT: Corine Vernet
;   APPLICANT: Meera Patturajan
;   TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;   FILE REFERENCE: 21402-593B
;   CURRENT APPLICATION NUMBER: US/10/637,313
;   CURRENT FILING DATE: 2003-08-08
;   PRIOR APPLICATION NUMBER: 10/162335
;   PRIOR FILING DATE: 2002-06-03
;   PRIOR APPLICATION NUMBER: 60/295607
;   PRIOR FILING DATE: 2001-06-04
;   PRIOR APPLICATION NUMBER: 60/295661
;   PRIOR FILING DATE: 2001-06-04
;   PRIOR APPLICATION NUMBER: 60/296404
;   PRIOR FILING DATE: 2001-06-06
;   PRIOR APPLICATION NUMBER: 60/296418
;   PRIOR FILING DATE: 2001-06-06
;   PRIOR APPLICATION NUMBER: 60/298285
;   PRIOR FILING DATE: 2001-06-14
;   PRIOR APPLICATION NUMBER: 60/298556
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/299949
;   PRIOR FILING DATE: 2001-06-21
;   PRIOR APPLICATION NUMBER: 60/300883
;   PRIOR FILING DATE: 2001-06-26
;   PRIOR APPLICATION NUMBER: 60/301550
;   PRIOR FILING DATE: 2001-06-28
Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 255
;   SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 20
;   TYPE: PRT
;   LENGTH: 398
;   ORGANISM: Homo sapiens
US-10-637-313-20

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Query Match       98.5%;   Score 660;   DB 5;   Length 398;
Best Local Similarity    100.0%;   Pred. No. 3.2e-61;
Matches   123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 283

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 343

Qy        123 LGM 125
              |||
Db        344 LGM 346
```

RESULT 9
US-09-919-039-29
Sequence 29, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
;   APPLICANT: Kaser, Matthew R.
;   TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;   FILE REFERENCE: PA-0035 US
;   CURRENT APPLICATION NUMBER: US/09/919,039
;   CURRENT FILING DATE: 2002-09-09
;   PRIOR APPLICATION NUMBER: 60/222,113
;   PRIOR FILING DATE: 2000-07-28
;   NUMBER OF SEQ ID NOS: 401
;   SOFTWARE: PERL Program
SEQ ID NO 29
;   LENGTH: 427
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
US-09-919-039-29

```
Query Match       98.5%;   Score 660;   DB 3;   Length 427;
Best Local Similarity    100.0%;   Pred. No. 3.5e-61;
Matches   123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 372

Qy        123 LGM 125
              |||
Db        373 LGM 375
```

RESULT 10
US-10-637-313-24
; Sequence 24, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khramtsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 24
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-24

Query Match   98.5%; Score 660; DB 5; Length 427;
Best Local Similarity   100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372

Qy 123 LGM 125
         |||
Db 373 LGM 375

RESULT 11
US-10-741-600-1179
; Sequence 1179, Application US/10741600

; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1179
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1179

Query Match   98.5%; Score 660; DB 5; Length 427;
Best Local Similarity   100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372

Qy 123 LGM 125
         |||
Db 373 LGM 375

RESULT 12
US-10-741-600-1181
; Sequence 1181, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1181
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1181

Query Match   98.5%; Score 660; DB 5; Length 427;
Best Local Similarity   100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372

Qy 123 LGM 125
         |||
Db 373 LGM 375

RESULT 13
US-10-893-315-101
; Sequence 101, Application US/10893315
; Publication No. US20050147987A1

GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
  TITLE OF INVENTION: USES THEREOF
  FILE REFERENCE: CL000786
  CURRENT APPLICATION NUMBER: US/10/893,315
  CURRENT FILING DATE: 2004-07-19
  PRIOR APPLICATION NUMBER: 60/231,397
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 2172
  SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 101
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-10-893-315-101

Query Match   98.5%;   Score 660;   DB 5;   Length 579;
Best Local Similarity   100.0%;   Pred. No. 5.2e-61;
Matches 123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 307

Qy 123 LGM 125
         |||
Db 308 LGM 310

RESULT 14
US-10-893-315-105
Sequence 105, Application US/10893315
Publication No. US20050147987A1
GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
  TITLE OF INVENTION: USES THEREOF
  FILE REFERENCE: CL000786
  CURRENT APPLICATION NUMBER: US/10/893,315
  CURRENT FILING DATE: 2004-07-19
  PRIOR APPLICATION NUMBER: 60/231,397
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 2172
  SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 105
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-10-893-315-105

Query Match   98.5%;   Score 660;   DB 5;   Length 579;
Best Local Similarity   100.0%;   Pred. No. 5.2e-61;
Matches 123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 247

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 248 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 307

Qy 123 LGM 125
         |||
Db 308 LGM 310

RESULT 15
US-10-162-335-72
Sequence 72, Application US/10162335
Publication No. US2004009480A1
GENERAL INFORMATION:
  APPLICANT: Anderson, David W.
  APPLICANT: Baumgartner, Jason C.
  APPLICANT: Boldog, Ferenc L.
  APPLICANT: Casman, Stacie J.
  APPLICANT: Edinger, Shlomit R.
  APPLICANT: Gangolli, Esha A.
  APPLICANT: Gerlach, Valerie
  APPLICANT: Gorman, Linda
  APPLICANT: Guo, Xiaojia (Sasha)
  APPLICANT: Hjalt, Tord
  APPLICANT: Kekuda, Ramesh
  APPLICANT: Li, Li
  APPLICANT: MacDougall, John R.
  APPLICANT: Malyankar, Uriel M.
  APPLICANT: Millet, Isabelle
  APPLICANT: Padigaru, Muralidhara
  APPLICANT: Patturajan, Meera
  APPLICANT: Pena, Carol E. A.
  APPLICANT: Rastelli, Luca
  APPLICANT: Shimkets, Richard A.
  APPLICANT: Stone, David J.
  APPLICANT: Spytek, Kimberly A.
  APPLICANT: Vernet, Corine A. M.
  APPLICANT: Voss, Edward Z.
  APPLICANT: Zerhusen, Bryan D.
  TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
  FILE REFERENCE: 21402-377 B
  CURRENT APPLICATION NUMBER: US/10/162,335
  CURRENT FILING DATE: 2002-10-01
  PRIOR APPLICATION NUMBER: 60/295,607
  PRIOR FILING DATE: 2001-06-04
  PRIOR APPLICATION NUMBER: 60/295,661
  PRIOR FILING DATE: 2001-06-04
  PRIOR APPLICATION NUMBER: 60/296,404
  PRIOR FILING DATE: 2001-06-06
  PRIOR APPLICATION NUMBER: 60/296,418
  PRIOR FILING DATE: 2001-06-06
  PRIOR APPLICATION NUMBER: 60/297,414
  PRIOR FILING DATE: 2001-06-11
  PRIOR APPLICATION NUMBER: 60/297,567
  PRIOR FILING DATE: 2001-06-12
  PRIOR APPLICATION NUMBER: 60/298,285
  PRIOR FILING DATE: 2001-06-14
  PRIOR APPLICATION NUMBER: 60/298,556
  PRIOR FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/299,949
  PRIOR FILING DATE: 2001-06-21
  PRIOR APPLICATION NUMBER: 60/300,883
  PRIOR FILING DATE: 2001-06-26
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 201
;
; SEQ ID NO 72
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-72

Query Match   98.5%;   Score 660;   DB 4;   Length 615;
Best Local Similarity   100.0%;   Pred. No. 5.6e-61;
Matches 123;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
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Db 224 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 283

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
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Db     284  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP  343

Qy     123  LGM  125
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Db     344  LGM  346
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Search completed: February 8, 2006, 03:21:54
Job time : 179 secs

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: February 8, 2006, 03:19:03 ; Search time 16 seconds
(without alignments)
91.547 Million cell updates/sec

Title: US-10-661-784-2
Perfect score: 670
Sequence: 1 GSGKDFVQPPTKICVGCPRD.........YVVPWEKKIYPTVNCQPLGM 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Published Applications AA_New:*
1: /cgn2_6/pcodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/pcodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/pcodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/pcodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/pcodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/pcodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/pcodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/pcodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	165.5	24.7	167	6	US-10-689-742-197	Sequence 197, App
2	136	20.3	148	6	US-10-967-093-8	Sequence 8, Appli
3	133.5	19.9	146	6	US-10-967-093-10	Sequence 10, Appli
4	130	19.4	140	6	US-10-967-093-6	Sequence 6, Appli
5	129.5	19.3	140	5	US-10-967-093-4	Sequence 4, Appli
6	129.5	19.3	382	6	US-09-978-360A-425	Sequence 425, App
7	127.5	19.0	146	6	US-10-982-545-4	Sequence 4, Appli
8	127.5	19.0	146	6	US-10-967-093-2	Sequence 2, Appli
9	110.5	16.5	97	6	US-10-821-234-1237	Sequence 1237, Ap
10	94.5	14.1	345	6	US-10-888-962-7	Sequence 7, Appli
11	91.5	13.7	352	6	US-10-888-962-8	Sequence 8, Appli
12	88.5	13.2	367	6	US-10-888-962-6	Sequence 6, Appli
13	82	12.2	758	6	US-10-467-962B-12	Sequence 12, Appli
14	74	11.0	138	6	US-11-137-465-37	Sequence 37, Appli
15	72	10.7	359	6	US-10-888-962-5	Sequence 5, Appli
16	69	10.3	1126	6	US-10-485-517-248	Sequence 248, Appl
17	67	10.0	198	7	US-11-169-041-223	Sequence 223, App
18	65	9.7	734	7	US-11-093-274-40	Sequence 40, Appl
19	65	9.7	1187	6	US-10-821-234-955	Sequence 955, App
20	63.5	9.5	162	7	US-11-215-658-8	Sequence 8, Appli
21	63.5	9.5	1597	6	US-10-877-346-41	Sequence 41, Appl
22	63.5	9.5	1641	6	US-11-074-176-40	Sequence 40, Appl
23	63	9.4	697	6	US-11-074-176-62	Sequence 62, Appl
24	62.5	9.3	449	7	US-11-169-041-138	Sequence 138, App
25	62	9.3	583	7	US-11-080-991-64	Sequence 64, Appl
26	62	9.3	1038	7	US-11-107-028-1	Sequence 1, Appli
27	61.5	9.2	384	7	US-11-075-351-12	Sequence 12, Appl
28	61.5	9.2	628	6	US-10-793-626-2844	Sequence 2844, Ap
29	61.5	9.2	1178	7	US-11-044-899-29	Sequence 29, Appl
30	61.5	9.2	1286	6	US-10-877-346-38	Sequence 38, Appl
31	61.5	9.2	2053	6	US-10-877-346-11	Sequence 11, Appl
32	61.5	9.2	2066	6	US-10-877-346-9	Sequence 9, App
33	61	9.1	227	6	US-10-485-517-210	Sequence 210, App
34	61	9.1	227	6	US-10-485-517-241	Sequence 241, App
35	61	9.1	1306	6	US-10-485-517-5406	Sequence 5406, App
36	60.5	9.0	334	7	US-11-016-564-1	Sequence 1, Appli
37	60.5	9.0	391	7	US-11-207-626A-30	Sequence 30, Appl
38	60.5	9.0	407	7	US-11-016-564-7	Sequence 7, Appli
39	60	9.0	603	7	US-11-183-136-2	Sequence 2, Appli
40	60	9.0	267	7	US-11-052-554A-300	Sequence 300, Appl
41	60	9.0	651	6	US-10-821-234-1666	Sequence 1666, Ap
42	59.5	8.9	193	6	US-09-978-360A-558	Sequence 558, App
43	59.5	8.9	481	6	US-10-995-561-959	Sequence 959, App
44	59	8.8	248	7	US-11-054-515-1386	Sequence 1386, App
45	59	8.8	932	7	US-11-057-058-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-10-689-742-197
Sequence 197, Application No. US10689742
Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 197
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-197

Query Match   24.7%; Score 165.5; DB 6; Length 167;
Best Local Similarity   32.5%; Pred. No. 1.6e-10;
Matches   37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

Qy   11 TKICVCGPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
          ::| |||| |: : :|: | : :|| ::| : | ::|:||| ::|| :|
Db   54 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 113

Qy   71 FVARETTCSKESNEELTESCE-----TKKLGQSLDCNAEVYYVVPWEKKI-YPTVNC 120
          |:: |: |: |: : ::| .|: |::| | :.:: || |: ||||||
Db   114 VEIGRTTCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC 166

RESULT 2
US-10-967-093-8
Sequence 8, Application US/10967093
Publication No. US20050267021A1
; GENERAL INFORMATION:
; APPLICANT: Schiemann, William P.
; TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
; FILE REFERENCE: 2879-104

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;   CURRENT APPLICATION NUMBER: US/10/967,093
;   CURRENT FILING DATE: 2004-10-15
;   PRIOR APPLICATION NUMBER: 60/511,794
;   PRIOR FILING DATE: 2003-10-15
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 8
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-967-093-8

Qy   24 NSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN 83
           :|| ||||||:|||||||||||||||||||||||||||||||:|::||||||||||||
Db   48 NEEGVQERALSFAVSEFNRKRSNDAYQSRVRVRVRVRARKQVVSGMNYFLDVELGRTTCTK-S 105

Qy   84 EELTESC------ETKKLGQSLDCNAEVYVVPWEKKKIYPTVN----CQ 121
           ::||| :      :||||||||||||||||||||||||:|:||    |:
Db  106 QANLDSCPFHNQPHLKREKL-----CSFQVYVVPWMN---TINLVKFSCQ 147
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RESULT 3
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US-10-967-093-10
; Sequence 10, Application US/10967093
; Publication No. US20050267021A1
; GENERAL INFORMATION:
;   APPLICANT: Schiemann, William P.
;   TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
;   FILE REFERENCE: 2879-104
;   CURRENT APPLICATION NUMBER: US/10/967,093
;   CURRENT FILING DATE: 2004-10-15
;   PRIOR APPLICATION NUMBER: 60/511,794
;   PRIOR FILING DATE: 2003-10-15
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 10
;   LENGTH: 146
;   TYPE: PRT
;   ORGANISM: Macaca mulatta
US-10-967-093-10

Query Match      19.9%;  Score 133.5;  DB 6;  Length 146;
Best Local Similarity  29.0%;  Pred. No. 3e-07;
Matches   31;  Conservative   21;  Mismatches 48;  Indels   7;  Gaps   3;

Qy    8 QPPPKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
           :||:| |||.|| ||:::|||||||||||||||||||||||||||||||:|||:||||
Db   31 KPPR--LVGGPMDASVEEEGVRRALDFAVSEYNKASNDMYHSRALQVRARKQIVAGVNY 88

Qy   68 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
           |.:|:|| :|| ::|:|:|||   :|||:|:|:|:|| |:| ::|
Db   89 FLDVELGRTTCTK--TQPNLDNCPFHEQPHLKRKAFCSFQIYTVPWQ 133
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RESULT 4
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US-10-967-093-6
; Sequence 6, Application US/10967093
; Publication No. US20050267021A1
; GENERAL INFORMATION:
;   APPLICANT: Schiemann, William P.
;   TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
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RESULT 5
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US-10-967-093-4
; Sequence 4, Application US/10967093
; Publication No. US20050267021A1
; GENERAL INFORMATION:
;   APPLICANT: Schiemann, William P.
;   TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
;   FILE REFERENCE: 2879-104
;   CURRENT APPLICATION NUMBER: US/10/967,093
;   CURRENT FILING DATE: 2004-10-15
;   PRIOR APPLICATION NUMBER: 60/511,794
;   PRIOR FILING DATE: 2003-10-15
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 4
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-967-093-4

Query Match      19.3%;  Score 129.5;  DB 6;  Length 140;
Best Local Similarity  30.0%;  Pred. No. 7.4e-07;
Matches   30;  Conservative   21;  Mismatches 44;  Indels   5;  Gaps   3;

Qy   15 VGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVAR 74
           :||||||||||||||||||||||||||||||||||||||||||||||||:|||||||.
Db   30 LGAPEEADANEEGVRRALDFAVSEYNKGSNDAYHSRAIQVVRARKQIVAGVNYFLDVEMG 89

Qy   75 ETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
           :|||||||||||||    :|:| ::|:|:|:|||||||||
Db   90 RTTCTK-SQTNLTD-CPFHDQPHLMRKALCSFQIYSVPWK 127
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RESULT 6
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US-09-978-360A-425
; Sequence 425, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
;   APPLICANT: Edwards, Jean-Baptiste Dumas Milne
;   APPLICANT: Duclert, Aymeric
;   APPLICANT: Bougueleret, Lydie
;   APPLICANT: Jobert, Severin
;   APPLICANT: Clubel, Catherine
;   TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
;   FILE REFERENCE: 56.US4.CIP
;   CURRENT APPLICATION NUMBER: US/09/978,360A
;   CURRENT FILING DATE: 2001-10-15
;   PRIOR APPLICATION NUMBER: US/09/978,360A
;   PRIOR FILING DATE: 1997-11-13
;   PRIOR APPLICATION NUMBER: US 60/066,677
;   PRIOR FILING DATE: 1997-11-13
;   PRIOR APPLICATION NUMBER: US 60/069,957
;   PRIOR FILING DATE: 1997-12-17
;   PRIOR APPLICATION NUMBER: US 60/074,121
;   PRIOR FILING DATE: 1998-02-09
;   PRIOR APPLICATION NUMBER: US 60/081,563
;   PRIOR FILING DATE: 1998-04-13
;
;   SEQ ID NO 6
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(Right-column alignment blocks)

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US-10-967-093-6

Query Match      20.3%;  Score 136;  DB 6;  Length 148;
Best Local Similarity  30.6%;  Pred. No. 1.6e-07;
Matches   34;  Conservative   22;  Mismatches 31;  Indels  24;  Gaps   5;
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US-10-967-093-10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-967-093-10

Query Match      19.9%;  Score 133.5;  DB 6;  Length 146;
Best Local Similarity  29.0%;  Pred. No. 3e-07;
Matches   31;  Conservative   21;  Mismatches 48;  Indels   7;  Gaps   3;
```

```
US-10-967-093-6

Qy    8 QPPPKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
Db   24 RPPPRL-LGAPQEADASEEGVQRALDFAVSEYNKGSNDAYHSRAIQVVRARKQLVAGINY 82

Qy   68 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
Db   83 YLDVEMGRTTCTK-SQTNLT-NCPFHDQPHLMRKALCSFQIYSVPWK 127
```

```
US-10-967-093-4

Qy    8 QPPPKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
Db   24 RPPPRL-LGAPQEADASEEGVQRALDFAVSEYNKGSNDAYHSRAIQVVRARKQIVAGVNY 82

Qy   68 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
Db   90 RTTCTCK-SQTNLTD-CPFHDQPHLMRKALCSFQIYSVPWK 127
```

```
US-09-978-360A-425

Qy   75 ETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
Db   90 RTTCTCK-SQTNLTD-CPFHDQPHLMRKALCSFQIYSVPWK 127
```

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; LENGTH: 140
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-967-093-6

Query Match      19.4%;  Score 130;  DB 6;  Length 140;
Best Local Similarity  28.0%;  Pred. No. 6.5e-07;
Matches   28;  Conservative   43;  Mismatches 43;  Indels   6;  Gaps   4;
```

```
;    PRIOR APPLICATION NUMBER: US 60/096,116
;    PRIOR APPLICATION FILING DATE: 1998-08-10
;    PRIOR APPLICATION NUMBER: US 60/099,273
;    PRIOR APPLICATION FILING DATE: -09-04
;    PRIOR APPLICATION NUMBER: US 09/191,997
;    PRIOR APPLICATION FILING DATE: 1998-11-13
;    PRIOR APPLICATION NUMBER: US 09/215,435
;    PRIOR APPLICATION FILING DATE: 1998-12-17
;    PRIOR APPLICATION NUMBER: PCT/IB98/02122
;    PRIOR APPLICATION FILING DATE: 1998-12-17
;    PRIOR APPLICATION NUMBER: US 09/247,155
;    PRIOR APPLICATION FILING DATE: 1999-02-09
;    Remaining Prior Application data removed - See File Wrapper or PALM.
;    NUMBER OF SEQ ID NOS: 810
;    SOFTWARE: Patent.pm
US-09-978-360A-425
;    LOCATION: -15..-1
;    NAME/KEY: SIGNAL
;    FEATURE:
;    ORGANISM: Homo sapiens
;    TYPE: PRT
;    LENGTH: 382
;  SEQ ID NO 425

Query Match     19.3%;  Score 129.5;  DB 5;  Length 382;
Best Local Similarity   30.4%;  Pred. No. 2.6e-06;
Matches  35;  Conservative  18;  Mismatches  43;  Indels  19;  Gaps   6;

Qy      14 CVGCPRDIPTNSP--ELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDF 71
           ::|:||  |:|:    :|::|  ||:|:::|:  ||::|  |: :::|::
Db     151 CPDCPSSIPTDSSNHQVLEAATESLAKYNNENTSKQY-SLFKVTRASSQWVVGPSYFVEY 209

Qy      72 VARETTCSKESNEELTESCETKKLGQSLD-----CNAEVYVPWEKKIYPTVNC 120
           : |  ::::|: :  :   |  :|:|  :     :|:||:  ||    :  |
Db     210 LIKESPCTKSQ----ASSCSL----QSSDSVPVGLCKGSLTRTHWEK--FVSVTC 254


RESULT 7
US-10-982-545-4
;    Sequence 4, Application US/10982545
;    Publication No. US20050248090A1
;    GENERAL INFORMATION:
;    APPLICANT: Davies, Huw Alun
;    APPLICANT: McGuire, James
;    APPLICANT: Simonsen, Anja Hviid
;    APPLICANT: Blennow, Kaj
;    APPLICANT: Podust, Vladimir
;    APPLICANT: Ciphergen Biosystems, Inc.
;    TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
;    FILE REFERENCE: 016866-0115S0US
;    CURRENT APPLICATION NUMBER: US/10/982,545
;    CURRENT FILING DATE: 2004-11-06
;    PRIOR APPLICATION NUMBER: US 60/518,360
;    PRIOR APPLICATION FILING DATE: 2003-11-07
;    PRIOR APPLICATION NUMBER: US 60/526,753
;    PRIOR APPLICATION FILING DATE: 2003-12-02
;    PRIOR APPLICATION NUMBER: US 60/546,423
;    PRIOR APPLICATION FILING DATE: 2004-02-19
;    PRIOR APPLICATION NUMBER: US 60/547,250
;    PRIOR APPLICATION FILING DATE: 2004-02-23
;    PRIOR APPLICATION NUMBER: US 60/558,896
;    PRIOR APPLICATION FILING DATE: 2004-04-02
;    PRIOR APPLICATION NUMBER: US 60/572,617
;    PRIOR APPLICATION FILING DATE: 2004-05-18
;    PRIOR APPLICATION NUMBER: US 60/586,503
;    PRIOR APPLICATION FILING DATE: 2004-07-08
;    NUMBER OF SEQ ID NOS: 16
;    SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 4
;    LENGTH: 146
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
```

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;    OTHER INFORMATION: Cystatin C precursor
;    FEATURE:
;    NAME/KEY: SIGNAL
;    LOCATION: (1)..(26)
;    OTHER INFORMATION: signal peptide
;    FEATURE:
;    NAME/KEY: PEPTIDE
;    LOCATION: (27)..(146)
;    OTHER INFORMATION: biomarker peptide M13391, full-length Cystatin C
;    OTHER INFORMATION: mature peptide
;    FEATURE:
;    NAME/KEY: PEPTIDE
;    LOCATION: (35)..(146)
;    OTHER INFORMATION: biomarker peptide M12583.4, truncated Cystatin C
US-10-982-545-4

Query Match     19.0%;  Score 127.5;  DB 6;  Length 146;
Best Local Similarity   28.0%;  Pred. No. 1.3e-06;
Matches  30;  Conservative  21;  Mismatches  49;  Indels   7;  Gaps   3;

Qy       8 QPPFKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
           :||   ||:||   |::
Db      31 KPPR--LVGGPMDASVEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNY 88

Qy      68 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
           :|| |:|
Db      89 FLDVELGRTTCTK--TQPNLDNCPFHDQPHLKRAFCSFQIYAVPWQ 133


RESULT 8
US-10-967-093-2
;    Sequence 2, Application US/10967093
;    Publication No. US20050267021A1
;    GENERAL INFORMATION:
;    APPLICANT: Schiemann, William P.
;    TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
;    FILE REFERENCE: 2879-104
;    CURRENT APPLICATION NUMBER: US/10/967,093
;    CURRENT FILING DATE: 2004-10-15
;    PRIOR APPLICATION NUMBER: 60/511,794
;    PRIOR APPLICATION FILING DATE: 2003-10-15
;    NUMBER OF SEQ ID NOS: 10
;    SOFTWARE: Patentin version 3.1
;  SEQ ID NO 2
;    LENGTH: 146
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-967-093-2

Query Match     19.0%;  Score 127.5;  DB 6;  Length 146;
Best Local Similarity   28.0%;  Pred. No. 1.3e-06;
Matches  30;  Conservative  21;  Mismatches  49;  Indels   7;  Gaps   3;

Qy       8 QPPFKICVGCPRDIPTNSPELEETLTHITTKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
Db      31 KPPR--LVGGPMDASVEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNY 88

Qy      68 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 111
Db      89 FLDVELGRTTCTK--TQPNLDNCPFHDQPHLKRAFCSFQIYAVPWQ 133


RESULT 9
US-10-821-234-1237
;    Sequence 1237, Application US/10821234
;    Publication No. US20050255114A1
;    GENERAL INFORMATION:
;    APPLICANT: Labat, Ivan
;    APPLICANT: Stache-Crain, Birgit
;    APPLICANT: Andaarmani, Susan
;    APPLICANT: Tang, Y. Tom
;    TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;    FILE REFERENCE: 821A
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; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
;
; SEQ ID NO 1237
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1237

Query Match   16.5%; Score 110.5; DB 6; Length 97;
Best Local Similarity   28.9%; Pred. No. 4.6e-05;
Matches 24; Conservative 19; Mismatches 35; Indels 5; Gaps 2;

Qy   32 LTHITHITKLNAENNATFYFKIDNYKKARVQVVAGKKYFIDFVARETTCSKESNEELTESC- 90
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||| :||
Db   4 LDFAVGEVNKASNDMYHSRALQVVRARKQIVAGVWNYFLDVELGRTTCTK--TQPNLDNCP 61

Qy   91 --ETKKLGQSLDCNAEVYVVPWE 111
            :|||:|:||:||:|||
Db   62 FHDQPHLRKRKAFCSPQIYAVPWQ 84

RESULT 10
US-10-888-962-7
; Sequence 7, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; TITLE OF INVENTION: Growth
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-888-962-7

Query Match   14.1%; Score 94.5; DB 6; Length 345;
Best Local Similarity   26.0%; Pred. No. 0.01;
Matches 25; Conservative 18; Mismatches 48; Indels 5; Gaps 3;

Qy   2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 61
          |:| :||||:||||||||||||||||||||||||||||||
Db   134 STPDSAEDVRKLCPRCPLITPFNDTNVHTVNTALAAFNTQNNGT-YFKLVEISRAQ-NV 191

Qy   62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQ 97
          :::||||||||||||||:|||||||||||||||||:
Db   192 PLPVSTLVEEVIAATDCTA---KEVTDPAKCNLLAE 224

RESULT 11
US-10-888-962-8
; Sequence 8, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; TITLE OF INVENTION: Growth
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-888-962-8

Query Match   13.7%; Score 91.5; DB 6; Length 352;
Best Local Similarity   27.1%; Pred. No. 0.022;
Matches 26; Conservative 17; Mismatches 48; Indels 5; Gaps 3;

Qy   2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 61
          |:| :||||:||||||||||||||||||||||||||||||
Db   134 STPDSAEDVRKFCPRCPLIIRFNDTNVHTVKTALAAFNAQNNGT-YFKLVEISRAQ-NV 191

Qy   62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQ 97
          :::||||||||||||||:|||||||||||||||||:
Db   192 PFPVSTLVEEVIAATDC---TGQEVTDPAKCNLLAE 224

RESULT 12
US-10-888-962-6
; Sequence 6, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; TITLE OF INVENTION: Growth
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-962-6

Query Match   13.2%; Score 88.5; DB 6; Length 367;
Best Local Similarity   26.1%; Pred. No. 0.048;
Matches 35; Conservative 22; Mismatches 56; Indels 21; Gaps 8;

Qy   2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 61
          |:| ||||:||||||||||||||||||||||||||||||
Db   134 SSPDSAEDVRKVCQDCPLLAPLNDTRVVHAAKALLAAFNRAQNNGS-NFQLBEISRAQLVP 192

Qy   62 VAGKKYFIDFVARETTC-SKESNEE-----LTES----CB----TKKLGQSLDCNAEVYVV 108
          :::|||||||||||| |::||| :|: |: ||||
Db   193 LPPSTY-VEFTVSGTDCVAKEATEAAAKCNLLAEKQYGFCKATLSEKLG-----GAEVAVT 246

Qy   109 PWEKKIYPTVNCQP 122
          :| ::||:||:|
Db   247 CTVFQTQP-VTSQP 259

RESULT 13
US-10-467-962B-12
; Sequence 12, Application US/10467962B

; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plösch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000_857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patentin Vers. 2.0
; SEQ ID NO 12
; LENGTH: 758
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-467-962B-12

Query Match   12.2%; Score 82; DB 6; Length 758;
Best Local Similarity   23.5%; Pred. No. 0.57;
Matches   32; Conservative 23; Mismatches   47; Indels   34; Gaps   5;

Qy   10 PTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKI--DNVKKARVQVVAGKK- 66
              |||| | | |||||| || ||| ||||| ||| | ||||| | | |||
Db   132 PALACLALARE----RPELLEMLSRRDVEVLVENGKPFLFKTGPDSLKRMSLYLRSGLQG 187

Qy   67 -------------YFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEV 105
                         || | |||| || | | ||| || ||
Db   188 IGKLMDMEKASTVDLMRLILSVVVDVASSEE--SKQHNKEIMESSVRSLLSQI----AKM 241

Qy   106 YVVPWEKKIYPTVNCQ 121
             | || | | ||
Db   242 SLRPPESNVHDTMQNQ 257

; Qy   19 RDIPTNSPELEETLTHTITKLNAENNATFYFKIDNV-KKARVQVVAGKKYFIDFVARETT 77
; |||| | ||||||||||||||||||||||||||| || | ||||||| |
; Db   35 QDIPQNYVVVQQALWFAMKEY---NKASFSITSSALGKEYKLKVTDSLEYYIEVKIARTI 91
;
; Qy   78 CSKESNEELTESCETKKLGQSLDCNAEVVVVPWE 111
; ||| | | | |||| |||| ||
; Db   92 CKKILSEDENCAFQEDPKMQKVVFCTFIVASKPWK 125

RESULT 14
us-11-137-465-37
; Sequence 37, Application US/11137465
; Publication No. US20050255558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kablick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 37
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-137-465-37

Query Match   11.0%; Score 74; DB 7; Length 138;
Best Local Similarity   24.5%; Pred. No. 0.47;
Matches   23; Conservative 20; Mismatches   47; Indels   4; Gaps   2;

RESULT 15
US-10-888-962-5
; Sequence 5, Application US/10888962
; Publication No. US20050265531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; TITLE OF INVENTION: Growth
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Bos taurus
; US-10-888-962-5

Query Match   10.7%; Score 72; DB 6; Length 359;
Best Local Similarity   22.8%; Pred. No. 2.5;
Matches   23; Conservative 16; Mismatches   48; Indels   14; Gaps   3;

Qy   2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 61
             | ||| || |||| | | |||||| || ||| ||||| ||| |
Db   134 SSPDSAEDVRKLCPDCPLLAPLNDSRVHAVEVALATFNAESNGS-YLQLVEISRAQ--- 189

Qy   62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCN 102
              || || | |||| || | | ||| ||
Db   190 --------FVPLPVSVSVEFAVAATD-CIAKEVVDPTKCN 220

Search completed: February 8, 2006, 03:22:16
Job time : 17 secs

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 8, 2006, 03:13:07 ; Search time 41 Seconds
(without alignments)
293.344 Million cell updates/sec

Title: US-10-661-784-2
Perfect score: 670
Sequence: 1 GSGKDFVQPPTKICVGCPRD............YVVPWBKKIYPTVNCQPLGM 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
    PIR_80:*
    1: pir1:*
    2: pir2:*
    3: pir3:*
    4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	660	98.5	427	1	KGHU1J	kininogen, LMW pre
2	644	98.5	644	1	KGHUH1	kininogen, HMW pre
3	477	71.2	436	1	KGBOL1	kininogen, LMW I p
4	477	71.2	621	1	KGBOH1	kininogen, HMW I p
5	450	67.2	434	1	KGBOL2	kininogen, LMW II
6	450	67.2	619	1	KGBOH2	kininogen, HMW II
7	426	63.6	433	2	A28055	K-kininogen, LMW I
8	426	63.6	639	2	A25486	kininogen, HMW I p
9	409	61.0	430	2	A23897	major acute phase
10	409	61.0	430	2	B28055	T-kininogen, LMW I
11	402	60.0	423	1	KGRTM	major acute phase
12	401	59.9	430	1	KGRTT1	T-kininogen I prec
13	136	20.3	112	1	UDBO	cystatin - bovine
14	133	19.9	91	2	S68035	T-kininogen (clone
15	133	19.9	91	2	S68034	T-kininogen (clone
16	130	19.4	127	2	S07085	cystatin C precurs
17	129	19.3	120	2	S15587	cystatin C - rat
18	128	19.1	111	2	A28793	cystatin C - puff ad
19	127.5	19.0	111	2	A36163	cystatin - puff ad
20	127.5	19.0	140	1	UDHU	cystatin C precurs
21	125	18.7	141	2	B29632	cystatin SA precur
22	118.5	17.7	139	1	UDCH	cystatin precursor
23	113.5	16.9	122	2	A43644	sarcocystatin A pr
24	113	16.9	141	1	JQ1470	cystatin precursor
25	111.5	16.6	111	2	JC2040	cystatin - chum sa
26	109.5	16.3	141	1	UDHUP2	cystatin SN precur
27	109	16.3	141	1	UDHUP1	cystatin S precurs
28	107.5	16.0	132	2	JC4918	cystatin S precurs
29	107	16.0	139	2	T33740	hypothetical prote
30	105.5	15.7	162	2	A43428	onchocystatin - ne
31	97.5	14.6	135	2	JC4007	cystatin II - maiz
32	97	14.5	133	2	JC4536	cystatin precursor
33	95.5	14.3	143	2	T33301	hypothetical prote
34	95	14.2	143	2	A47142	cystatin D precurs
35	94.5	14.1	345	2	S21094	alpha-2-HS-glycopr
36	93.5	14.0	139	2	A45361	cystatin-related e
37	92	13.7	100	2	JH0269	cystatin - avocado
38	91.5	13.7	135	2	S27239	fetuin precursor -
39	91.5	13.7	375	2	A32827	alpha-2-HS-glycopr
40	88.5	13.2	125	2	T00752	cystatin - maize
41	88.5	13.2	134	2	JC4882	cystatin - avocado
42	88.5	13.2	134	2	S54828	cysteine proteinas
43	88.5	13.2	367	1	WOHU	cystatin - field m
44	85	12.7	199	2	S65071	alpha-2-HS-glycopr
45	84.5	12.6	592	2	T50516	Ca2+ dependent lip

ALIGNMENTS

RESULT 1
KGHU1J
KGHU1J
kininogen, LMW precursor [validated] - human
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1982 #sequence revision 27-Nov-1985 #text change 09-Jul-2004
C;Accession: A01280; B25276; A27900; A27699; A31905; A34030
R;Ohkubo, I.; Kurachi, K.; Takagawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23 5691-5697, 1984
A;cross-references: UNIPROT:P01042; UNIPARC:UPI0000000D92C;
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identi
A;Reference number: A90490; MUID:85122621; PMID:6441591
A;Molecule type: mRNA
A;Residues: 1-427 <TAK>
A;Cross-references: UNIPARC:UPI0000000D92C; GB:M11437; NID:g186751; PIDN:AAB59551.1; PID
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W.
in Kinin IV, Part A, Greenbaum, L.M., and Margolius, H.S., eds., pp.91-95, Plenum, New
A;Title: Amino acid sequence of the light chain of human low molecular mass kininogen.
A;Reference number: A27900
A;Molecule type: protein
A;Residues: 1-427 <OHK>
A;cross-references: UNIPROT:P01042; UNIPARC:UPI0000000D92C; GB:K02566; NID:g177889; PIDN
J;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A;Reference number: A92544; MUID:85234582; PMID:2989293
A;Molecule type: mRNA
A;Accession: B25276
A;Residues: 390-427 <LOT>
A;cross-references: UNIPARC:UPI0001742A0
R;Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A;Title: A new kinin moiety in human plasma kininogens.
A;Reference number: A27699; MUID:88209021; PMID:3365237
A;Accession: A27699
A;Molecule type: protein
A;Residues: 380-389 <MIN>
A;Cross-references: UNIPARC:UPI0000002C0F8
R;Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic flu
A;Reference number: A31905; MUID:89034061; PMID:3182782
A;Accession: A31905
A;Molecule type: protein
A;Residues: 381-389 <MAR>
A;Cross-references: UNIPARC:UPI0000002CF4A
R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human plas
A;Reference number: A34030; MUID:88106632; PMID:3337729

A;Accession: A34030
A;Molecule type: protein
A;Residues: 380-389 <SAS>
A;Cross-references: UNIPARC:UPI000002C0F8
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti
A;Reference number: A92545; MUID:85234583; PMID:2989294
A;Contents: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622; PMID:4952632
A;Contents: annotation; bradykinin
A;Contents: The LMW kininogen precursor is produced from the same gene as the HMW form (e
C;Comment: kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Genetics:
A;Gene: GDB:KNG
A;Cross-references: GDB:125256; OMIM:228960
A;Map position: 3q27-3q27
C;Superfamily: kininogen; cystatin homology
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-427/Product: LMW prokininogen (kininogen I) #status predicted <MAT>
F;19-379/Product: LMW kininogen II #status predicted <MAT2>
F;19-379,390-427/Product: LMW kininogen heavy chain #status predicted <HCH>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin I) #status experimental <KBDY>
F;380-427/Product: bradykinin (kallidin II) #status experimental <BDY>
F;381-389/Product: LMW kininogen light chain #status experimental <LCH>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;28-407,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:
F;48,169,205,294/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F;383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;401/Binding site: carbohydrate (Thr) (covalent) #status absent

Query Match   98.5%; Score 660; DB 1; Length 427;
Best Local Similarity   100.0%; Pred. No. 7.8e-55;
Matches 123; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQVV  62
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Db  253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKSENEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
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Qy  123 LGM 125
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Db  373 LGM 375
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RESULT 2
KGHUH1

Kininogen, HMW precursor [validated] - human
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
N;Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular we
C;Species: Homo sapiens (man)
A;Molecule type: protein
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004
C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030; S02
R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identi
A;Reference number: A90490; MUID:85122621; PMID:6441591

A;Molecule type: mRNA
A;Residues: 1-389 <OHK>
A;Cross-references: UNIPROT:P01042; UNIPARC:UPI000017429G; GB:K02566; NID:g177809
R;Kitamura, N.; Kitagawa, H.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A;Reference number: A92544; MUID:85234582; PMID:2989293
A;Accession: A25276
A;Molecule type: mRNA
A;Residues: 1-592,'I',594-644 <TAK>
A;Cross-references: UNIPARC:UPI0000135DAC; GB:M11437; NID:g186751; PIDN:AAB59550.1; PID
R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain 3.
A;Reference number: S32422; MUID:93223854; PMID:8467916
A;Accession: S32422
A;Molecule type: mRNA
A;Residues: 253-377 <AUE>
A;Cross-references: UNIPARC:UPI000174297
A;Note: differences are due to known cloning artifacts
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kinino
A;Reference number: A91153; MUID:86030270; PMID:4054110
A;Accession: A91153
A;Molecule type: protein
A;Residues: 379-644 <LOT>
A;Cross-references: UNIPARC:UPI000174298
A;Note: the bradykinin sequence preceding the light chain sequence was not determined i
R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Biochem. 154, 471-478, 1986
A;Title: Completion of the primary structure of human high-molecular-mass kininogen. Th
A;Reference number: A24871; MUID:86108361; PMID:3484703
A;Accession: A24871
A;Molecule type: protein
A;Residues: 'Z',20-380 <KEL1>
A;Cross-references: UNIPARC:UPI000174299
R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp. 85-89, Plenum Press, New Yo
A;Title: Amino acid sequence of the light chain of human high molecular mass kininogen.
A;Reference number: A27899
A;Accession: A27899
A;Molecule type: protein
A;Residues: 379-389,'K',390-407,'Q',409-644 <KEL2>
A;Cross-references: UNIPARC:UPI00001429A
R;Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A;Title: A new kinin moiety in human plasma kininogens.
A;Reference number: A27699; MUID:88209021; PMID:3365237
A;Accession: A27699
A;Molecule type: protein
A;Residues: 380-389 <MIN>
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R;Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic flu
A;Reference number: A31905; MUID:89034061; PMID:3182782
A;Accession: A31905
A;Molecule type: protein
A;Residues: 381-389 <MAE>
R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human pla
A;Reference number: A34030; MUID:88106632; PMID:3337729
A;Accession: A34030
A;Molecule type: protein
A;Residues: 380-389 <SAS>
A;Cross-references: UNIPARC:UPI000002C0F8
R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory an
A;Reference number: S02482; MUID:89076517; PMID:3264507

A;Accession: S02482
A;Molecule type: protein
A;Residues: 1-19;189-192;310-314;381-389 <LEN1>
A;Cross-references: UNIPARC:UPI000002CF4A; UNIPARC:UPI0000143284; UNIPARC:UPI000017429B;
R;Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues of bradykinin in human
A;Reference number: A61495; MUID:88211869; PMID:3366244
A;Accession: A61495
A;Molecule type: protein
A;Residues: 380-389 <KAT1>
A;Cross-references: UNIPARC:UPI000002CF08
A;Experimental source: urine
A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
A;Accession: B61495
A;Molecule type: protein
A;Residues: 380-389 <KAT2>
A;Cross-references: UNIPARC:UPI000002CF08
A;Experimental source: urine
A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
A;Accession: S14447
A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like
A;Reference number: S68059; MUID:96033974; PMID:7589467
A;Accession: S68059
A;Molecule type: protein
A;Residues: 264-359,'N',361-375 <LEN>
R;Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation and examination of substrate-spec
A;Accession: S55239
A;Molecule type: protein
A;Residues: 450-452,'X',454,'X',456 <LIT>
R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A;Reference number: S14303; MUID:91192133; PMID:2013314
A;Accession: S14303
A;Molecule type: protein
A;Residues: 431-434 <STR>
A;Cross-references: UNIPARC:UPI000017429F
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti
A;Reference number: A92545; MUID:85234583; PMID:2989294
A;Contents: annotation: gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622; PMID:4952632
A;Contents: annotation: bradykinin

C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor <SIG>
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Genetics:
A;Gene: KNG
A;Cross-references: GDB:125256; OMIM:228960
A;Map position: 3q27-3q27
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C;Superfamily: kininogen; cystatin homology
F;1-18/Domain: signal sequence experimental <SIG>
F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>

F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <LCH>
F;390-644/Domain: kininogen light chain #status experimental <LCH>
F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F;431-434/Product: low molecular weight growth promoting factor #status experimental <Gl
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
F;28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:
F;48/Binding site: carbohydrate (Asn) (covalent) #status absent
F;169,205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;379-380/Cleavage site: Met-Lys (kallikrein) (partial) #status experimental
F;383/Modified site: 4-hydroxyproline (Pro) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;401,533,542,546,557,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status exp
F;577/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match   98.5%; Score 660; DB 1; Length 644;
Best Local Similarity   100.0%; Pred. No. 1.2e-54;
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Db 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
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Db 313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 372

Qy 123 LGM 125
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Db 373 LGM 375

RESULT 3
KGBO11
kininogen, LMW I precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A01283
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors an
A;Reference number: A93984; MUID:83117859; PMID:6572010
A;Accession: A01283
A;Molecule type: mRNA
A;Residues: 1-436 <NAW>
A;Cross-references: UNIPROT:P01046; UNIPARC:UPI00001ZDF24; GB:J00010; GB:V00426; NID:g16
A;Comment: The LMW kininogen precursor is produced from the same gene as the HMW form an
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, '
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; gly
C;Superfamily: kininogen; cystatin homology
F;1-18/Domain: signal sequence experimental <SIG>
F;19-436/Product: LMW kininogen I #status predicted <MAT>
F;19-130/Domain: LMW kininogen I heavy chain #status predicted <HCH>
F;19-131/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>
F;379-388/Domain: lysyl-bradykinin (kallidin II) #status predicted <KBDY>
F;380-388/Product: bradykinin (kallidin I) #status predicted <LCH>
F;389-436/Product: LMW kininogen II light chain #status experimental <LCH>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) <LCH>
F;27-406,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds:
F;47,87,168,169,197,204/Binding site: carbohydrate (Asn) #status predicted
F;378-379/Cleavage site: Met-Lys (kallikrein) #status predicted
F;382/Modified site: 4-hydroxyproline (Pro) #status predicted
F;388-389/Cleavage site: Arg-Ser (kallikrein) #status predicted

Query Match
Best Local Similarity 71.2%;   Score 477; DB 1; Length 436;
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Db     373 G 373

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Db     313 GLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTVNCQPL 372

Qy     253 KDFVQPPTRLCAGCPKPIPVDSPDLEEPLSHSIAKLNAEHDGAFYFKIDTVKKATVQVVA 312
Qy       4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA  63
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RESULT 4
KGBOH1
kininogen, HMW I precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
A;Accession: A01281
A;Molecule type: mRNA
A;Residues: 1-621 <KIT>
A;Cross-references: UNIPROT:P01044; UNIPARC:UPI000012DF1C; GB:V01491; GB:K01757; NID:949
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
A;Accession: A01281; A91923; A91938; A29559
R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
N;Title: A single gene for bovine high molecular weight and low molecular weight kininog
J;Nature 305, 545-549, 1983
A;Reference number: A93317; MUID:84014106; PMID:6571699
A;Accession: A01281
A;Molecule type: mRNA
A;Residues: 1-621 <KIT>
A;Cross-references: UNIPARC:UPI000012DF1C; GB:V01491; GB:K01757; NID:949
R;Kato, H.; Nagasawa, S.; Suzuki, T.
J;Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
A;Reference number: A91923; MUID:70180420; PMID:4986212
A;Accession: A91923
A;Molecule type: protein
A;Residues: 378-393 <KAT>
A;Cross-references: UNIPARC:UPI000017A2A1
R;Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
J;Biochem. 77, 55-68, 1975
N;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami
A;Reference number: A91938; MUID:75170265; PMID:1169237
A;Molecule type: protein
A;Residues: 458-498 <HAN>
R;Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga,
J;Biol. Chem. 262, 2768-2779, 1987
A;Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of c
A;Reference number: A92627; MUID:87137530; PMID:3546295
A;Accession: A29559
A;Molecule type: protein
A;Residues: 'Z',20-123,'I',125-127,'I',129-378 <SUE>
A;Cross-references: UNIPARC:UPI000017A2A3
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Müller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kininog
A;Reference number: A91153; MUID:86030270; PMID:4054110
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984
A;Title: Disulfide bonds in bovine HMW kininogens.
A;Reference number: A94300
A;Contents: annotation; disulfide bonds
A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-379/Product: HMW kininogen I heavy chain #status predicted <MAT>
F;19-621/Product: HMW prokininogen I #status predicted <HCH>
F;141-252/Domain: cystatin homology <CY1>
F;263-374/Domain: cystatin homology <CY2>
F;380-388/Product: bradykinin (kallidin) #status experimental <KBDY>
F;380-621/Product: HMW kininogen I light chain #status experimental <BDY>
F;389-621/Product: HMW kininogen I light chain #status experimental <LCH>
F;417-488/Region: glycine/histidine/lysine-rich
F;Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds:
F;87,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;378-379/Cleavage site: Met-Lys (kallikrein) #status predicted
F;382/Modified site: 4-hydroxyproline (Pro) #status experimental
F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;398,405,512/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;399,400,520,524,536,548,553,570/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;498-499/Cleavage site: Arg-Thr (kallikrein) #status experimental

Query Match
Best Local Similarity 71.2%;   Score 477; DB 1; Length 621;
            71.9%; Pred. No. 2.5e-37;
Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

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Qy      64 GKKYFIDFVARETTCSKSENEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPL 123
           | ||| ::|||||||| |||||| :||| :  | : |||:|||||||| :|||||||||
Db     313 GLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTVNCQPL 372

Qy       4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA  63
Db     253 KDFVQPPTRLCAGCPKPIPVDSPDLEEPLSHSIAKLNAEHDGAFYFKIDTVKKATVQVVA 312

Qy     124 G 124
           |
Db     373 G 373
```

RESULT 5
KGBOL2
kininogen, LMW II precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen II; prokininogen
A;Accession: A01284
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
A;Accession: A01284
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors an
A;Reference number: A93904; MUID:83117859; PMID:6572010
A;Accession: A01284
A;Molecule type: mRNA
A;Residues: 1-434 <NAW>
A;Cross-references: UNIPROT:P01047; UNIPARC:UPI000012DF28; GB:V00427; GB:J00011; NID:94
C;Comment: The LMW kininogen precursor is produced from the same gene as the HMW form a
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of th
C;Comment: Bradykinin, released from kininogen prior to the release of bradykinin.
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: blood coagulation; cysteine proteinase inhibitor; g]
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-130/Domain: cystatin homology <CY1>
F;19-377/Product: LMW kininogen II #status predicted <HCH>
F;19-434/Product: LMW kininogen II heavy chain #status predicted <MAT>
F;130-252/Domain: cystatin homology <CY2>
F;141-252/Domain: cystatin homology <CY3>
F;261-372/Domain: cystatin homology <CY3>
F;377-386/Product: lysyl-bradykinin (kallidin) #status predicted <KBDY>
F;378-386/Product: bradykinin (kallidin) #status predicted <BDY>
F;387-434/Product: LMW kininogen I light chain #status experimental <LCH>

```
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;27-404,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
F;47,87,168,169,197,204,280/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;376-377/Cleavage site: Met-Lys (kallikrein) #status predicted
F;380/Modified site: 4-hydroxyproline (Pro) #status predicted
F;386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted
```

Query Match   67.2%; Score 450; DB 1; Length 434;
Best Local Similarity   68.9%; Pred. No. 6.2e-35;
Matches 84; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

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Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKINAENNATFYFKIDNVKKARVQVV 62
Db 252 GEDFL--PPMVCVGCPKPIPVDSPDLEEALNHSIAKLNAEHDGTFYFKIDTVKKATVQVV 309

Qy  63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVPWEKKIYPTVNCQP 122
Db 310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVVVPWEEKVYPTVNCQP 369

Qy 123 LG 124
Db 370 LG 371
```

RESULT 6

KGBOH2
HMW II precursor - bovine
A;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Alternate names: bradykinin (kallidin I; kininogen I; kininogen II; preprokininogen
N;Contains bradykinin (kallidin I; kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A01282; A91923; A91941; A91938; B29559
R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
Nature 305, 545-549, 1983
A;Title: A single gene for bovine high molecular weight and low molecular weight kininog
A;Reference number: A93317; MUID:84014106; PMID:6571699
A;Accession: A01282
A;Molecule type: mRNA
A;Residues: 1-619 <KIT>
A;Cross-references: UNIPROT:P01045; UNIPARC:UPI000012DF1F; GB:V01492; GB:K01758; NID:g49
R;Kato, H.; Nagasawa, S.; Suzuki, T.
J;Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
A;Reference number: A91923; MUID:70180420; PMID:4986212
A;Accession: A91923
A;Molecule type: protein
A;Residues: 376-391 <KAT>
A;Cross-references: UNIPARC:UPI0000174A1
R;Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
J;Biochem. 79, 1201-1222, 1976
A;Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino a
A;Reference number: A91941; MUID:76260155; PMID:956151
A;Accession: A91941
A;Molecule type: protein
A;Residues: 387-455 <HAN>
A;Cross-references: UNIPARC:UPI0000174A4
A;Note: 398-Pro, 401-Val, and 455-Lys were also found
R;Han, Y.N.; Koniya, M.; Iwanaga, S.; Suzuki, T.
J;Biochem. 77, 55-68, 1975
A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami
A;Reference number: A91938; MUID:75170265; PMID:1169237
A;Accession: A91938
A;Molecule type: protein
A;Residues: 456-496 <HA2>
A;Cross-references: UNIPARC:UPI0000174A2
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J;Biol. Chem. 262, 2768-2779, 1987
A;Title: Primary structure of the mRNAs encoding the rat precursors for bradykinin and
nhibitor.
A;Reference number: A92627; MUID:87137530; PMID:3546295
A;Accession: B29559
A;Molecule type: protein
A;Residues: 2,20-104,'B',106-256,'XX',257-376 <SUE>
A;Cross-references: UNIPARC:UPI00001742A5

R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kinino
A;Reference number: A91153; MUID:86030270; PMID:4054110
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984
A;Title: Disulfide bonds in bovine HMW kininogens.
A;Reference number: A94300
A;Contents: annotation; disulfide bonds
A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form a
C;Comment: Kininogen is a cysteine proteinase inhibitor; takes part in initiation of th
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is imp
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator,
xyproline residue is present in the sequence prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keyword: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dup
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19/Product: HMW kininogen II #status predicted <MAT>
F;19-376/Product: HMW kininogen II heavy chain #status experimental <HCH>
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;261-372/Domain: cystatin homology <CY3>
F;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
F;387-619/Product: HMW kininogen II light chain #status experimental <LCH>
F;418-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
F;87,168,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status absent
F;136/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;376-377/Cleavage site: Met-Lys (kallikrein) #status experimental
F;380/Modified site: 4-hydroxyproline (Pro) #status predicted
F;386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;397,400,404,510/Binding site: carbohydrate (Ser) (covalent) #status e
F;397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status e
F;496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental
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Query Match    67.2%;  Score 450;  DB 1;  Length 619;
Best Local Similarity   68.9%;  Pred. No. 9.1e-35;
Matches 84;  Conservative 14;  Mismatches 22;  Indels 2;  Gaps 1;

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Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKINAENNATFYFKIDNVKKARVQVV 62
Db 252 GEDFL--PPMVCVGCPKPIPVDSPDLEEALNHSIAKLNAEHDGTFYFKIDTVKKATVQVV 309

Qy  63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVPWEKKIYPTVNCQP 122
Db 310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVVVPWEEKVYPTVNCQP 369

Qy 123 LG 124
Db 370 LG 371
```

RESULT 7

A28055
K;Kininogen, LMW I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28055
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J;Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
nhibitor.
A;Reference number: A92496; MUID:86008264; PMID:2413018
A;Accession: A28055
A;Molecule type: mRNA
A;Residues: 1-433 <FUR>
A;Cross-references: UNIPROT:P08934; UNIPARC:UPI000017A66

C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence
F;19-433/Product: K-kininogen, LMW I
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>

```
Query Match             63.6%;  Score 426; DB 2;  Length 433;
Best Local Similarity   65.0%;  Pred. No. 1.2e-32;
Matches  80;  Conservative  14;  Mismatches  29;  Indels  0;  Gaps  0;

Qy     3 GKDFVQPPTKICVGCPRDIPTNSPELEEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||| ||  | || ||||| || |||||:  | : |::|||||||:  ||||| |||| ||
Db   253 GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTTFYFKIDTVKKATSQVV 312

Qy    63 AGKKYFIDFVARETTCSKSESNEELTESCETTKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
           || ||:|:||| || |||||||  || |  | :|||||| ||| || : | |  ||||| :
Db   313 AGTKYVIEFIARETNCSKSESNAELTADCETKRLGQSLNCNANVYMRPWENKVVPTVKCKV 372

Qy   123 LGM 125
           | |
Db   373 LDM 375
```

RESULT 8
A25486
kininogen, HMW I precursor - rat
N;Contains: bradykinin
A;Molecule type: mRNA
A;Residues: 1-639 <KIT>
A;Cross-references: UNIPROT:P08934; UNIPARC:UPI00001DF1B
A;Note: the authors translated the codon CAA for residue 347 as Asn
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C;Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number; A92625; MUID:87137443; PMID:3029068

```
Query Match             65.0%;  Score 426; DB 2;  Length 639;
Best Local Similarity   65.0%;  Pred. No. 1.8e-32;
Matches  80;  Conservative  14;  Mismatches  29;  Indels  0;  Gaps  0;

Qy     3 GKDFVQPPTKICVGCPRDIPTNSPELEEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||| ||  | || ||||| || |||||:  | : |::|||||||:  ||||| |||| ||
Db   253 GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTTFYFKIDTVKKATSQVV 312

Qy    63 AGKKYFIDFVARETTCSKSESNEELTESCETTKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
           || ||:|:||| || |||||||  || |  | :|||||| ||| || : | |  ||||| :
Db   313 AGTKYVIEFIARETNCSKSESNAELTADCETKRLGQSLNCNANVYMRPWENKVVPTVKCKV 372

Qy   123 LGM 125
           | |
Db   373 LDM 375
```

RESULT 9
A23897
major acute phase alpha-1 protein (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A23897; B23897
R;Anderson, K.P.; Heath, E.C.

J. Biol. Chem. 260, 12065-12071, 1985
A;Title: The relationship between rat major acute phase protein and the kininogens.
A;Reference number: A23897; MUID:86008266; PMID:2413019
A;Accession: A23897
A;Residues: 1-14 <AND1>
A;Cross-references: UNIPROT:P01048; UNIPARC:UPI00000177A63
A;Accession: B23897
A;Residues: 5-430 <AND2>
A;Molecule type: mRNA
A;Residues: 5-430 <AND2>
A;Cross-references: UNIPROT:P01048; UNIPARC:UPI0000177A0C; GB:M11661; NID:g205307; PIDN:AAA41570.1; PID:g205307; PID:
A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415
A;Superfamily: kininogen; cystatin homology
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>

```
Query Match             61.0%;  Score 409; DB 2;  Length 430;
Best Local Similarity   61.8%;  Pred. No. 4.7e-31;
Matches  76;  Conservative  15;  Mismatches  32;  Indels  0;  Gaps  0;

Qy     3 GKDFVQPPTKICVGCPRDIPTNSPELEEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
           ||| |   | | ||||:||| |||||:  | : |::||| ::|: ||||| |||| ||
Db   252 GDDLFSLLPKKCFCGCPKNIPVDSPELKEALGHSIAQLNAQHNLFYFKIDTVKKATSQVA 311

Qy    63 AGKKYFIDFVARETTCSKSESNEELTESCETTKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
           || ||:|:||| || |||||  :  ||| |  :| |||| ||| || : | |  ||||| :
Db   312 AGTKYVIEFIARETNCSKSESKQTNTELTADCETHGLGQSLNCNANVYMRPWENKVVPTVRCQA 371

Qy   123 LGM 125
           | |
Db   372 LDM 374
```

RESULT 10
B28055
T-kininogen, LMW II precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28055; E25486; B28526; C28526
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kininogen.
inhibitor.
A;Reference number: A92496; MUID:86008264; PMID:2413018
A;Accession: B28055
A;Molecule type: mRNA
A;Residues: 1-430 <FUR>
A;Cross-references: UNIPROT:P08932; UNIPARC:UPI000012DF30
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:87137443; PMID:3029068
A;Accession: E25486
A;Molecule type: DNA
A;Residues: 375-430 <KIT>
A;Cross-references: UNIPARC:UPI00000003E0
R;Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A;Title: Purification and characterization of rat T-kininogens isolated from plasma of
A;Reference number: A92729; MUID:88087226; PMID:3121623
A;Accession: B28526
A;Residues: 'E',20-48,376-430 <ENJ>
A;Molecule type: protein
A;Residues: 'E',20-25,'MD',28-48,376-430 <EN2>
A;Cross-references: UNIPARC:UPI0000177A67
A;Accession: C28526
A;Molecule type: protein
A;Residues: 'E',20-48;376-388,'R',390-419,'ER',422-430 <EN3>
A;Cross-references: UNIPARC:UPI00000177A67
A;Accession: C28526
C;Superfamily: kininogen; cystatin homology
C;Keywords: glycoprotein; kininogen; cystatin homology
C;Keywords: pyroglutamic acid
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-430/Product: T-kininogen, LMW II #status experimental <MAT>

P;19-130/Domain: cystatin homology <CY1>
P;141-252/Domain: cystatin homology <CY2>
P;263-374/Domain: cystatin homology <CY3>
P;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
P;82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #statu

```
Query Match           61.0%;  Score 409;  DB 2;  Length 430;
Best Local Similarity 61.8%;  Pred. No. 4.7e-31;
Matches         76;  Conservative  15;  Mismatches  32;  Indels  0;  Gaps  0;

Qy        3  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  62
             |||||    | || || ||   ||:.:|| ||:.|||.: |||||:||||||||||||||
Db      252  GDDLFSLLPKKCFGCPKNIPVDSPELKEALGHSIARLNAQHNHLFYFKIDTVKKATSQVV  311

Qy       63  AGKKYFPIDFVAREETTCSKESNEELTESCETKKLGQSLDCNABVYVVPWEKKIIYPTVNCQP  122
             |:|||||||||||||||||| :| ||||:||  ::::||||||||||||||||||||||:|
Db      312  AGTKYVIEFIARETNCSKQTNTELITADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA  371
```

Qy   123 LGM 125
             |||
Db   372 LDM 374

RESULT 11
KGRTM
major acute phase alpha-1 protein precursor - rat (fragment)
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
R;Cole, T.; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
FEBS Lett. 182, 57-61, 1985
A;Title: Major acute phase alpha1-protein of the rat is homologous to bovine kiningen a
A;Reference number: A01285
A;Accession: A01285
A;Molecule type: mRNA
A;Residues: 1-423 <COL>
A;Cross-references: UNIPARC:UPI000001742A6
C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflamma
r
C;Superfamily: kininogen; cystatin homology
C;Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam
F;1-11/Domain: signal sequence (fragment) #status predicted <SIG>
F;12-423/Product: major acute phase alpha-1 protein #status predicted <MAT>
F;12-123/Domain: cystatin homology <CV1>
F;134-245/Domain: cystatin homology <CV2>
F;256-367/Domain: cystatin homology <CV3>
F;12/Product: bradykinin #status predicted <BDY>
F;371-379/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;161,197/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match           60.0%;  Score 402;  DB 1;  Length 423;
Best Local Similarity 61.8%;  Pred. No. 2.1e-30;
Matches         76;  Conservative  14;  Mismatches  33;  Indels  0;  Gaps  0;

Qy        3  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV  62
             |||||    | || || ||   ||:.:|| ||:.|||.: |||||:|||||||| |||||
Db      245  GDDLFELLPKNCRCGCPREIPVDSPELKEALGHSIARLNAQHNHIFYFKLDTVKKATSQVV  304

Qy       63  AGKKYFPIDFVAREETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIIYPTVNCQP  122
             |:|||||||||||||||||| :| ||||:||  ::::||||||||||||| |||||||:|
Db      305  AGVIYVIEFIARETNCSKQSKTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA  364
```

Qy   123 LGM 125
             |||
Db   365 LDM 367

RESULT 12
KGRTT1
T-kininogen I precursor - rat
N;Alternate names: 73K protein; LMW kininogen T-I

(right column)

N;Contains: bradykinin; T-kinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 31-Dec-2004
C;Accession: A01286; D25486; A28526; PL0193; JQ0027; B25488; A28525; S68036
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
nhibitor.
A;Reference number: A92496; MUID:86008264; PMID:2413018
A;Accession: A01286
A;Molecule type: mRNA
A;Residues: 1-430 <FUR>
A;Cross-references: UNIPARC:UPI0000000E7F29
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:87137443; PMID:3029068
A;Accession: D25486
A;Molecule type: DNA
A;Residues: 375-430 <KIT>
A;Cross-references: UNIPARC:UPI0000000E7F29
R;Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A;Title: Purification and characterization of rat T-kininogens isolated from plasma of
A;Reference number: A92729; MUID:88087226; PMID:3121623
A;Accession: A28526
A;Molecule type: protein
A;Residues: 'E',20-48;376-430 <ENJ>
R;Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A;Title: Identification of a protein increasing in serum of Nagase analbuminemic rats b
A;Reference number: PL0193; MUID:90216390; PMID:2108948
A;Accession: PL0193
A;Molecule type: mRNA
A;Residues: 330-420, 'R',422-429, 'P' <KAN>
A;Cross-references: UNIPARC:UPI000001742A9
R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding rat T-kininogen.
A;Reference number: JQ0027; MUID:90034172; PMID:2806908
A;Accession: JQ0027
A;Molecule type: DNA
A;Residues: 1-60, 'E',62-113, 'R',115-165, 'F',167-178, 'TKI',182-211, 'F',213-256, 'S',258-3
A;Cross-references: UNIPARC:UPI000001742AA
R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation sites of rat K an
A;Reference number: A25488; MUID:87137465; PMID:3818598
A;Accession: B25488
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-48 <KAG>
R;Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 965-972, 1988
A;Title: Purification and characterization of two kinds of low molecular weight kininog
A;Reference number: A28525; MUID:88087225; PMID:3335530
A;Accession: A28525
A;Molecule type: protein
A;Residues: 376-430 <EN2>
A;Cross-references: UNIPARC:UPI000001742A8
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of ag
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68036
A;Molecule type: mRNA
A;Residues: 340-430 <SIE>
A;Cross-references: UNIPARC:UPI000001742AB
C;Comment: At least three types of LMW kininogen precursors are present in rat plasma, t

ceding bradykinin.
C;Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after t
d of an Arg or Lys, it is probably not released from its precursor by either tissue or p
C;Comment: The T-kininogens are produced in response to an inflammatory stimulant.
C;Genetics:
A;Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
A;Superfamily: cystatin homology
C;Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glycopr
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-430/Product: T-kininogen I #status
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>
F;378-386/Product: bradykinin #status predicted <BDY>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;19/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;141-430/Product: T-kininogen I #status experimental <MAT>
F;205-217,263-266,327-339,350-369/Disulfide bonds: #status predicted
F;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status

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Query Match      59.9%;   Score 401; DB 1; Length 430;
Best Local Similarity    61.8%;   Pred. No.2.2e-30;
Matches   76;   Conservative   14;   Mismatches   33;   Indels    0;   Gaps    0;

Qy     3  GKDFVQPPPKICVGCPRDIPTNSPELEEETLTHTITIKLNAENNATFYFKIDNVKKARVQVV   62
Db   252  GDDLFELLPKNCRGCPREIPVDSPELKEALGHSIAQLNAQHNHIFYFKIDTVKKATSQVV   311

Qy    63  AGKKYFIDFVARETTCSKESENEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP  122
Db   312  AGVIVIEFIARETNCSKQSKTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA   371

Qy   123  LGM  125
Db   372  LDM  374
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RESULT 13
UDB0
cystatin - bovine
N;Alternate names: thiol proteinase inhibitor
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 06-Dec-1996
A;Accession: A01271
R;Hirado, M.; Tsunasawa, S.; Sakiyama, F.; Niinobe, M.; Fujii, S.
FEBS Lett. 186, 41-45, 1985
A;Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase in
A;Reference number: A01271; MUID:85231205; PMID:3891407
A;Accession: A01271
A;Molecule type: protein
A;Superfamily: cystatin; cystatin homology
A;Cross-references: UNIPARC:UPI000017J259
C;Superfamily: colostrum; cystatin; cystatin proteinase inhibitor
C;Keywords: colostrum; cystatin; cystatin proteinase inhibitor
F;2-112/Domain: cystatin homology <CYS>
F;48-52/Region: inhibitory #status predicted
F;66-76,90-110/Disulfide bonds: #status predicted

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Query Match      20.3%;   Score 136; DB 1; Length 112;
Best Local Similarity    30.6%;   Pred. No.7.7e-06;
Matches   34;   Conservative   22;   Mismatches   31;   Indels   24;   Gaps    5;

Qy    24  NSPELEEETLTHTITIKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN   83
Db    12  NEEGVQEALSFAVSEFNKRSNDAYQSRVRVRVRARKQVVSGMNYFLDVELGRTTCTK--S   69

Qy    84  EELTESC------------ETKKLGQSLDCNAEVYVVPWEKKIYPTVN-----CQ  121
Db    70  QANLDSCPFHNQPHLKREKL----CSFQVVVPWMN----TINLVKFSCQ  111
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C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 31-Dec-2004
C;Accession: S68035
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of agi
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68035
A;Molecule type: mRNA
A;Residues: 1-91 <SIE>
A;Cross-references: UNIPROT:063581; UNIPARC:UPI0000177A5F
A;Experimental source: liver
A;Superfamily: cystatin homology
C;Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

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Query Match      19.9%;   Score 133; DB 2; Length 91;
Best Local Similarity    68.6%;   Pred. No.1.2e-05;
Matches   24;   Conservative   3;   Mismatches   8;   Indels   0;   Gaps   0;

Qy    91  ETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM  125
Db     1  ETKHLGQSLNCNANVYMRPWENKVVPTVRCQALDM  35
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RESULT 14
S68035
T-kininogen (clone pSG17) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)

RESULT 15
S68034
T-kininogen (clone pSG22) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 31-Dec-2004
A;Accession: S68034
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of ag
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68034
A;Molecule type: mRNA
A;Residues: 1-91 <SIE>
A;Cross-references: UNIPROT:P70517; UNIPARC:UPI000017A5F
A;Experimental source: liver
A;Superfamily: cystatin homology
C;Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

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Query Match      19.9%;   Score 133; DB 2; Length 91;
Best Local Similarity    68.6%;   Pred. No.1.2e-05;
Matches   24;   Conservative   3;   Mismatches   8;   Indels   0;   Gaps   0;

Qy    91  ETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM  125
Db     1  ETKHLGQSLNCNANVYMRPWENKVVPTVRCQALDM  35
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Search completed: February 8, 2006, 03:17:56
Job time : 42 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: February 8, 2006, 03:09:37 ; Search time 252 Seconds
                                                     (without alignments)
                                                     349.964 Million cell updates/sec

Title:
Perfect Score: 670
Sequence: 1 GSGKDFVQPPTKICVGCPRD..........YVVPWEKKIYPTVNCQPLGM 125

Sequence: US-10-661-784-2

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: BLOSUM62

Total number of hits satisfying chosen parameters: 2166443

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt.05.80:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

Searched: 2166443 seqs, 705528306 residues

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	660	98.5	427	2	Q53EQ0_HUMAN	Q53eq0 homo sapien
2	660	98.5	427	1	Q6PAU9_HUMAN	Q6pau9 homo sapien
3	660	98.5	644	1	KNG1_HUMAN	P01042 homo sapien
4	477	71.2	621	1	KNG1_BOVIN	P01044 bos taurus
5	450	67.2	619	2	KNG2_BOVIN	P01045 bos taurus
6	434	64.8	480	2	Q6S9I1_MOUSE	Q6s911 mus musculu
7	434	64.8	661	1	KNG1_MOUSE	Q6s911 mus musculu
8	426	63.6	433	2	Q5M8A0_RAT	P08677 mus musculu
9	426	63.6	639	1	KNG1_RAT	Q5m8a0 rattus norv
10	425	63.4	433	2	Q6S9T0_MOUSE	P08934 rattus norv
11	425	63.4	462	2	Q6S9I0_MOUSE	Q6s9t0 mus musculu
12	425	63.4	644	2	Q6S9I3_MOUSE	Q6s9i0 mus musculu
13	409	61.0	430	2	KNT2_RAT	Q6s913 mus musculu
14	409	61.0	430	2	Q5M894_RAT	P08932 rattus norv
15	404	60.3	140	2	Q7RP6_PIG	Q5m894 rattus norv
16	401	59.9	430	1	KNT1_RAT	Q7rp6 sus scrofa
17	401	59.9	430	2	Q5PQU1_RAT	P01048 rattus norv
18	399	59.6	430	2	Q63581_RAT	Q5pqu1 rattus norv
19	364	54.3	335	2	Q6DMP4_MOUSE	Q63581 rattus norv
20	176	26.3	335	2	Q4STD5_TETNG	Q6dmp4 mus musculu
21	175	26.1	144	1	CYTF_MOUSE	Q4std5 tetraodon n
22	175	26.1	167	2	Q9QWL5_MOUSE	O89098 mus musculu
23	173	25.8	392	2	Q5HZU6_XENTR	Q9qwl5 mus musculu
24	165.5	24.7	145	1	CYTF_HUMAN	Q5hzu6 xenopus tro
25	165.5	24.7	145	2	Q6FH95_HUMAN	O76096 homo sapien
26	165	24.6	331	2	Q5XJ76_BRARE	Q6fh95 homo sapien
27	165	24.6	146	2	Q5M8F3_XENTR	Q5xj76 brachydanio
28	155.5	23.2	138	2	Q4S2M6_TETNG	Q5m8f3 xenopus tro
29	152.5	22.8	462	2	Q7SYH2_XENLA	Q4s2m6 tetraodon n
30	152.5	22.8	462	2	Q7ZY91_XENLA	Q7syh2 xenopus lae
31	152.5	22.8	465	2	Q80IE5_XENLA	Q7zy91 xenopus lae
32	152.5	22.8	586	2	Q5XKA7_XENLA	Q80ie5 xenopus lae
33	148.5	22.2	318	2	Q4SMM7_TETNG	Q5xka7 xenopus lae
34	138.5	20.7	149	1	CYTM_HUMAN	Q4smm7 tetraodon n
35	138.5	20.7	149	2	Q61BD2_HUMAN	Q15828 homo sapien
36	138.5	20.7	149	2	Q540N7_HUMAN	Q61bd2 homo sapien
37	136	20.3	148	2	CYTC_BOVIN	Q540n7 homo sapien
38	136	20.3	148	2	Q54A26_BOVIN	P01035 bos taurus
39	133.5	19.9	146	1	CYTC_MACMU	Q54a26 bos taurus
40	132.5	19.8	146	2	Q6T6T4_BITGA	O19093 macaca mula
41	131	19.6	140	2	Q66L07_XENLA	Q6t6t4 bitis gabon
42	131	19.6	146	2	Q66L07_XENLA	O66107 xenopus lae
43	130	19.4	127	1	CYTC_RAT	P14841 rattus norv
44	130	19.4	140	2	Q5M968_RAT	Q5m968 rattus norv
45	129.5	19.3	140	1	CYTC_MOUSE	P21460 mus musculu

ALIGNMENTS

RESULT 1
Q53EQ0_HUMAN
ID   Q53EQ0_HUMAN PRELIMINARY;   PRT;   427 AA.
AC   Q53EQ0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Kininogen 1 variant (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT   "Construction and characterization of a full length-enriched and a 5'-
RT   end-enriched cDNA library.";
RL   Gene 200:149-156(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK223589; BAD97309.1; -; mRNA.
FT   NON_TER   1
SQ   SEQUENCE   427 AA; 47853 MW; C8B5A5F00BEDBBB9 CRC64;

Query Match   98.5%;   Score 660;   DB 2;   Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 62
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Db   253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVYVPWEKKIYPTVNCQP 122
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVYVPWEKKIYPTVNCQP 372

Qy   123 LGM 125
              |||
Db   373 LGM 375

RESULT 2

ID   Q6PAU9_HUMAN   PRELIMINARY;   PRT;   427 AA.
AC   Q6PAU9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Kininogen 1.
GN   Name=KNG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR   EMBL; BC060039; AAH60039.1; -; mRNA.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
SQ   SEQUENCE   427 AA; 47901 MW; 17DB6C2346D75912 CRC64;

Query Match   98.5%; Score 660; DB 2; Length 427;
Best Local Similarity   100.0%; Pred. No. 2.2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQVV 62
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Db   253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATYFKIDNVKKARVQVV 312

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372

Qy   123 LGM 125
             |||
Db   373 LGM 375

RESULT 3
ID   KNG1_HUMAN   STANDARD;   PRT;   644 AA.
AC   P01042; P01043;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Kininogen-1 precursor (Alpha-2-thiol proteinase inhibitor) (Contains:
DE   Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-bradykinin
DE   (Kallidin II); Kininogen-1 light chain; Low molecular weight growth
DE   promoting factor].
GN   Name=KNG1; Synonyms=BDK, KNG;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RX   MEDLINE=85122621; PubMed=6441591;
RA   Ohkubo I., Kurachi K., Takasawa T., Shiokawa H., Sasaki M.;
RT   "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and
RT   its identity with low molecular weight kininogen.";
RL   Biochemistry 23:5691-5697(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORMS HMW AND LMW).
RC   TISSUE=Liver;
RX   MEDLINE=85234582; PubMed=2989293;
RA   Takagaki Y., Kitamura N., Nakanishi S.;
RT   "Cloning and sequence analysis of cDNAs for human high molecular
RT   weight and low molecular weight prekininogens. Primary structures of
RT   two human prekininogens.";
RL   J. Biol. Chem. 260:8601-8609(1985).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS SER-163; THR-178 AND
RP   PRO-212.
RA   Rieder M.J., da Ponte S.H., Kuldanek S.A., Rajkumar N., Smith J.D.,
RA   Toth E.J., Nickerson D.A.;
RT   "The amino acid sequence of the light chain of human high-molecular-
RT   mass kininogen.";
RL   Eur. J. Biochem. 152:307-314(1985).
RN   [4]
RA   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   PROTEIN SEQUENCE OF 381-389.
RX   MEDLINE=90255622; PubMed=4952632;
RA   Pierce J.V.;
RT   "Structural features of plasma kinin and kininogens.";
RL   Fed. Proc. 27:52-57(1968).
RN   [6]
RP   PROTEIN SEQUENCE OF 19-380, CARBOHYDRATE-LINKAGE SITES ASN-169 AND
RP   ASN-205, AND ABSENCE OF CARBOHYDRATE AT ASN-48.
RX   MEDLINE=86108361; PubMed=3484703;
RA   Kellermann J., Lottspeich F., Henschen A., Muller-Esterl W.;
RT   "Completion of the primary structure of human high-molecular-mass
RT   kininogen. The amino acid sequence of the entire heavy chain and
RT   evidence for its evolution by gene triplication.";
RL   Eur. J. Biochem. 154:471-478(1986).
RN   [7]
RP   PROTEIN SEQUENCE OF 380-389, AND HYDROXYLATION SITE PRO-383.
RX   MEDLINE=88211869; PubMed=3366244; DOI=10.1016/0014-5793(88)80427-7;
RA   Kato H., Matsumura Y., Maeda H.;
RT   "Isolation and identification of hydroxyproline analogues of
RT   bradykinin in human urine.";
RL   FEBS Lett. 232:252-254(1988).
RN   [8]
RP   PROTEIN SEQUENCE OF 431-434, AND MASS SPECTROMETRY.
RX   MEDLINE=96033974; PubMed=7589467; DOI=10.1016/0014-5793(95)01037-F;
RA   Straczek J., Maachi F., Le Nguyen D., Becchi M., Heulin M.H.,
RA   Nabet P., Belleville F.;
RT   "Purification from human plasma of a tetrapeptide that potentiates
RT   insulin-like growth factor-I activity in chick embryo cartilage.";
RL   FEBS Lett. 373:207-211(1995).

```
RN   [9]
RP   GENE STRUCTURE.
RX   MEDLINE=85234583; PubMed=2989294;
RA   Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T.,
RA   Nakanishi S.;
RT   "Structural organization of the human kininogen gene and a model for
RT   its evolution.";
RL   J. Biol. Chem. 260:8610-8617(1985).
RN   [10]
RP   DISULFIDE BONDS.
RA   Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
RT   "Disulfide bonds in bovine HMW kininogens.";
RL   Seikagaku 56:808-808(1984).
RN   [11]
RP   AMINO-ACID COMPOSITION OF 381-389, AND HYDROXYLATION SITE PRO-383.
RX   MEDLINE=89034061; PubMed=3182782;
RA   Maeda H., Matsumura Y., Kato H.;
RT   "Purification and identification of [hydroxyprolyl3]bradykinin in
RT   ascitic fluid from a patient with gastric cancer.";
RL   J. Biol. Chem. 263:16051-16054(1988).
RN   [12]
RP   CARBOHYDRATE-LINKAGE SITE ASN-294.
RX   MEDLINE=22660472; PubMed=12754519; DOI=10.1038/nbt827;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
RN   [13]
RP   CARBOHYDRATE-LINKAGE SITES ASN-169 AND ASN-294, AND MASS SPECTROMETRY.
RX   PubMed=14760718; DOI=10.1002/pmic.200300556;
RA   Bunkenborg J., Pilch B.J., Podtelejnikov A.V., Wisniewski J.R.;
RT   "Screening for N-glycosylated proteins by liquid chromatography mass
RT   spectrometry.";
RL   Proteomics 4:454-465(2004).
CC   -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
CC       HMW-kininogen plays an important role in blood coagulation by
CC       helping to position optimally prekallikrein and factor XI next to
CC       factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-
CC       induced aggregation of thrombocytes; (4) the active peptide
CC       bradykinin that is released from HMW-kininogen shows a variety of
CC       physiological effects: (4A) influence in smooth muscle
CC       contraction, (4B) induction of hypotension, (4C) natriuresis and
CC       diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC       mediator of inflammation and causes (4E1) increase in vascular
CC       permeability, (4E2) stimulation of nociceptors (4E3) release of
CC       other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC       a cardioprotective effect (directly via bradykinin action,
CC       indirectly via endothelium-derived relaxing factor action); (5)
CC       LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC       kininogen is in contrast to HMW-kininogen not involved in blood
CC       clotting.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=HMW;
CC         IsoId=P01042-1; Sequence=Displayed;
CC       Name=LMW;
CC         IsoId=P01042-2; Sequence=VSP_001261, VSP_001262;
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC   -!- PTM: Hydroxylation of Pro-383 occurs prior to the release of
CC       bradykinin.
CC   -!- SIMILARITY: Contains 3 cystatin-like domains.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; K02566; AAA35497.1; -; mRNA.
DR   EMBL; M11437; AAB59550.1; -; Genomic_DNA.
DR   EMBL; M11438; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11521; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11522; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11523; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11525; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11526; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11527; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11528; AAB59550.1; JOINED; Genomic_DNA.
DR   EMBL; M11437; AAB59551.1; -; Genomic_DNA.
DR   EMBL; M11438; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11521; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11522; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11523; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11524; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11525; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11526; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11527; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; M11528; AAB59551.1; JOINED; Genomic_DNA.
DR   EMBL; AY248697; AAO61092.1; -; Genomic_DNA.
DR   PIR; A01279; KGHUHI.
DR   PIR; A01280; KGHUH1.
DR   SWISS-2DPAGE; P01042; HUMAN.
DR   Ensembl; ENSG00000113889; Homo sapiens.
DR   HGNC; HGNC:6383; KNG1.
DR   MIM; 228960; -.
DR   Reactome; P01042; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0008201; F:heparin binding; NAS.
DR   GO; GO:0005102; F:receptor binding; IPI.
DR   GO; GO:0008270; F:zinc ion binding; NAS.
DR   GO; GO:0030146; P:diuresis; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0030147; P:natriuresis; TAS.
DR   GO; GO:0030195; P:negative regulation of blood coagulation; IDA.
DR   GO; GO:0007162; P:negative regulation of cell adhesion; IDA.
DR   GO; GO:0043065; P:positive regulation of apoptosis; NAS.
DR   GO; GO:0006939; P:smooth muscle contraction; TAS.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00034; KININOGEN.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
KW   Alternative splicing; Blood coagulation; Bradykinin;
KW   Direct protein sequencing; Glycoprotein; Hydroxylation;
KW   Inflammatory response; Plasma; Polymorphism; Protease inhibitor;
KW   Pyrrolidone carboxylic acid; Repeat; Signal; Thiol protease inhibitor;
KW   Vasoactive; Vasodilator.
FT   SIGNAL        1     18
FT   CHAIN        19    644       Kininogen-1.
```

RESULT 4

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KNG1_BOVIN
ID   KNG1_BOVIN     STANDARD;      PRT;   621 AA.
AC   P01044; P01046;
DT   21-JUL-1986 (Rel. 01, Created)
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Query Match             98.5%;  Score 660;  DB 1;  Length 644;
Best Local Similarity   100.0%;  Pred. No. 3.4e-53;
Matches  123;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVVPWEKKIYPTVNCQP 372

Qy        123 LGM 125
              |||
Db        373 LGM 375
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DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Kininogen-1 precursor (Kininogen I) (Thiol proteinase inhibitor)
DE   [Contains: Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-
DE   bradykinin (Kallidin II); Kininogen-1 light chain].
GN   Name=KNG1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM I).
RX   MEDLINE=84014106; PubMed=6571699;
RA   Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RT   "A single gene for bovine high molecular weight and low molecular
RT   weight kininogens.";
RL   Nature 305:545-549(1983).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM HMW).
RX   MEDLINE=83117859; PubMed=6572010;
RA   Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RT   "Primary structures of bovine liver low molecular weight kininogen
RT   precursors and their two mRNAs.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RX   MEDLINE=87177530; PubMed=3546295;
RA   Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA   Miyata T., Iwanaga S.;
RT   "Bovine high molecular weight kininogen. The amino acid sequence,
RT   positions of carbohydrate chains and disulfide bridges in the heavy
RT   chain portion.";
RL   J. Biol. Chem. 262:2768-2779(1987).
RN   [4]
RP   PROTEIN SEQUENCE OF 378-393.
RX   MEDLINE=70180420; PubMed=4986212;
RA   Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
RT   "Studies on the primary structure of bovine high-molecular-weight
RT   kininogen. Amino acid sequence of a fragment ('histidine-rich
RT   peptide') released by plasma kallikrein.";
RL   J. Biochem. 77:55-68(1975).
RN   [5]
RP   PROTEIN SEQUENCE OF 19-378, AND CARBOHYDRATE-LINKAGE SITES ASN-87;
RP   ASN-168; ASN-169; ASN-197 AND ASN-204.
RX   MEDLINE=75170265; PubMed=1169237;
RA   Kato H., Nagasawa S., Suzuki T.;
RT   "Studies on the structure of bovine kininogen: cleavages of disulfide
RT   bonds and of methionyl bonds in kininogen-II.";
RL   J. Biochem. 67:313-323(1970).
CC   -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
CC       HMW-kininogen plays an important role in blood coagulation by
CC       helping to position optimally prekallikrein and factor XI next to
CC       factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-
CC       induced aggregation of thrombocytes; (4) the active peptide
CC       bradykinin that is released from HMW-kininogen shows a variety of
CC       physiological effects: (4A) influence in smooth muscle
CC       contraction, (4B) induction of hypotension, (4C) natriuresis and
CC       diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC       mediator of inflammation and causes (4E1) increase in vascular
CC       permeability, (4E2) stimulation of nociceptors (4E3) release of
CC       other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC       a cardioprotective effect (directly via bradykinin action,
CC       indirectly via endothelium-derived relaxing factor action); (5)
CC       LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC       kininogen is in contrast to HMW-kininogen not involved in blood
CC       clotting.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=HMW;
CC         IsoId=P01044-1; Sequence=Displayed;
CC       Name=LMW;
CC         IsoId=P01044-2; Sequence=VSP_013562, VSP_013563;
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC   -!- SIMILARITY: Contains 3 cystatin-like domains.
```

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DR   EMBL; V01491; CAA24735.1; -; mRNA.
DR   EMBL; V00426; CAA23709.1; -; mRNA.
DR   PIR; A01283; KGBOB1.
DR   PIR; A01281; KGBOH1.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00334; KININOGEN.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
KW   Alternative splicing; Blood coagulation; Bradykinin;
KW   Direct protein sequencing; Glycoprotein; Inflammatory response;
KW   Plasma; Protease inhibitor; Pyrrolidone carboxylic acid; Repeat;
KW   Signal; Thiol protease inhibitor; Vasoactive; Vasodilator.
FT   SIGNAL          1      18       Probable.
FT   CHAIN          19     621       Kininogen-1.
FT   CHAIN          19     378       Kininogen-1 heavy chain.
FT   PEPTIDE       379     388       Lysyl-bradykinin.
FT   PEPTIDE       380     388       Bradykinin.
FT   CHAIN         389     621       Kininogen-1 light chain.
FT   DOMAIN         19     135       Cystatin-like 1.
FT   DOMAIN        136     257       Cystatin-like 2.
FT   DOMAIN        258     378       Cystatin-like 3.
FT   SITE          197     197       Cleavage (by kallikrein).
FT   SITE          204     204       Cleavage (by kallikrein).
FT   SITE          378     379       Cleavage (by kallikrein).
FT   SITE          388     389       Cleavage (by kallikrein).
FT   SITE          498     499       Cleavage (by kallikrein).
FT   MOD_RES        19      19       Pyrrolidone carboxylic acid.
FT   CARBOHYD       87      87       N-linked (GlcNAc...).
FT   CARBOHYD      136     136       N-linked (GlcNAc...).
FT   CARBOHYD      168     168       N-linked (GlcNAc...); partial.
FT   CARBOHYD      169     169       N-linked (GlcNAc...).
FT   CARBOHYD      197     197       N-linked (GlcNAc...).
FT   CARBOHYD      204     204       N-linked (GlcNAc...).
FT   CARBOHYD      398     398       O-linked (GalNAc...).
FT   CARBOHYD      399     399       O-linked (GalNAc...).
FT   CARBOHYD      400     400       O-linked (GalNAc...); partial.
FT   CARBOHYD      406     406       O-linked (GalNAc...).
FT   CARBOHYD      512     512       O-linked (GalNAc...).
FT   CARBOHYD      520     520       O-linked (GalNAc...).
FT   CARBOHYD      524     524       O-linked (GalNAc...).
FT   CARBOHYD      536     536       O-linked (GalNAc...).
FT   CARBOHYD      548     548       O-linked (GalNAc...).
FT   CARBOHYD      553     553       O-linked (GalNAc...).
FT   CARBOHYD      570     570       O-linked (GalNAc...).
FT   DISULFID       27     591       Interchain (between heavy and light
FT                                   chains).
FT   DISULFID       82      93
FT   DISULFID      106     125
FT   DISULFID      141     144
FT   DISULFID      205     217
FT   DISULFID      228     247
FT   DISULFID      263     266
FT   DISULFID      327     339
FT   DISULFID      350     369
FT   VARSPLIC      401     436       VSLPHSAMSPVQDEERDSGKEBQGPTHGHGWDHGKQI ->
FT                                   HVRKSCEYKGRPEAGAEPAPQGEVSLPAESPQLAR (in
FT                                   isoform LMW).
FT                                   /FTId=VSP_013562.
FT   VARSPLIC      437     621       Missing (in isoform LMW).
FT                                   /FTId=VSP_013563.
FT   CONFLICT      295     295       A -> T (in Ref. 2).
SQ   SEQUENCE   621 AA;  68890 MW;  D16850BEFE3C55CD CRC64;
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Query Match    71.2%;  Score 477;  DB 1;  Length 621;
Best Local Similarity   71.9%;  Pred. No. 4.6e-36;
Matches  87;  Conservative  14;  Mismatches  20;  Indels  0;  Gaps  0;

Qy          4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA 63
              ||||||||:|.:|||:|  :  |.:|.||  ||||:.:|:| |.|||||||||  |||||
Db        253 KDFVQPPTRLCAGCKPIPVDSPDLEEPLSHSIAKLNAEHDGAFYFKIDTVKKAATVQVVA 312

Qy         64 GKKYFIDFVARETTCSKESNEELTESCETKLLGQSLDCNAEVYVVPWEKKIYPTVNCQPL 123
              |||:||||||||||||  : |||||  || |  :| |  ||||||||||||||||||||||
Db        313 GLKYSIVFIARETTCSKGSNEELTKSCEINHGQILHCDANVYVVPWEEKVYPTVNCQPL 372

Qy        124 G 124
              |
Db        373 G 373
```

RESULT 5

KNG2_BOVIN

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ID   KNG2_BOVIN    STANDARD;    PRT;   619 AA.
AC   P01045; P01047;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Kininogen-2 precursor (Kininogen II) (Thiol proteinase inhibitor)
DE   [Contains: Kininogen-2 heavy chain; Bradykinin (Kallidin II); Lysyl-
DE   bradykinin (Kallidin II); Kininogen-2 light chain].
GN   Name=KNG2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM HMW).
RX   MEDLINE=84014106; PubMed=6571699;
RA   Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RT   "A single gene for bovine high molecular weight and low molecular
RT   weight kininogens.";
RL   Nature 305:545-549(1983).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RX   MEDLINE=83117859; PubMed=6572010;
RA   Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RT   "Primary structures of bovine liver low molecular weight kininogen
RT   precursors and their two mRNAs.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
RN   [3]
RP   PROTEIN SEQUENCE OF 19-376, AND CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=87137530; PubMed=3542295;
RA   Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA   Miyata T., Iwanaga S.;
RT   "Bovine high molecular weight kininogen. The amino acid sequence,
RT   positions of carbohydrate chains and disulfide bridges in the heavy
RT   chain portion.";
RL   J. Biol. Chem. 262:2768-2779(1987).
RN   [4]
RP   PROTEIN SEQUENCE OF 376-391.
RX   MEDLINE=70180420; PubMed=4986212;
RA   Kato H., Nagasawa S., Suzuki T.;
RT   "Studies on the structure of bovine kininogen: cleavages of disulfide
RT   bonds and of methionyl bonds in kininogen-II.";
RL   J. Biochem. 67:313-323(1970).
RN   [5]
RP   PROTEIN SEQUENCE OF 387-455.
RX   MEDLINE=76260155; PubMed=956151;
RA   Han Y.N., Kato H., Iwanaga S., Suzuki T.;
RT   "Primary structure of bovine plasma high-molecular-weight kininogen.
RT   The amino acid sequence of bovine high molecular weight kininogen.
RT   following the C-terminus ot the bradykinin moiety.";
RL   J. Biochem. 79:1201-1222(1976).
RN   [6]
```

```
CC   -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
CC       HMW-kininogen plays an important role in blood coagulation by
CC       helping to position optimally prekallikrein and factor XI next to
CC       factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-
CC       induced aggregation of thrombocytes; (4) the active peptide
CC       bradykinin that is released from HMW-kininogen shows a variety of
CC       physiological effects: (4A) influence in smooth muscle
CC       contraction, (4B) induction of hypotension, (4C) natriuresis and
CC       diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC       mediator of inflammation and causes (4E1) increase in vascular
CC       permeability, (4E2) stimulation of nociceptors (4E3) release of
CC       other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC       a cardioprotective effect (directly via bradykinin action,
CC       indirectly via endothelium-derived relaxing factor action); (5)
CC       LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC       kininogen is in contrast to HMW-kininogen not involved in blood
CC       clotting.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=HMW;
CC         IsoId=P01045-1; Sequence=Displayed;
CC       Name=LMW;
CC         IsoId=P01045-2; Sequence=VSP_013564, VSP_013565;
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC   -!- SIMILARITY: Contains 3 cystatin-like domains.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; V01492; CAA24736.1; -; mRNA.
DR   EMBL; V00427; CAA23710.1; -; mRNA.
DR   PIR; A01282; KGBOH2.
DR   PIR; A01284; KGBOL2.
DR   HSSP; P01038; 1A90.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00334; KININOGEN.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
KW   Alternative splicing; Blood coagulation; Bradykinin;
KW   Direct protein sequencing; Glycoprotein; Hydroxylation;
KW   Inflammatory response; Plasma; Protease inhibitor;
KW   Pyrrolidone carboxylic acid; Repeat; Signal; Thiol protease inhibitor;
KW   Vasoactive; Vasodilator.
FT   SIGNAL        1     18
FT   CHAIN        19    619       Kininogen-2.
FT   CHAIN        19    376       Kininogen-2 heavy chain.
FT   PEPTIDE     377    386       Lysyl-bradykinin.
FT   PEPTIDE     378    386       Bradykinin.
FT   CHAIN       387    619       Kininogen-2 light chain.
FT   DOMAIN       19    135       Cystatin-like 1.
FT   DOMAIN      136    256       Cystatin-like 2.
FT   DOMAIN      257    376       Cystatin-like 3.
FT   SITE         47     47       Not glycosylated.
```

FT   SITE   376   377   Cleavage (by kallikrein).
FT   SITE   386   387   Cleavage (by kallikrein).
FT   SITE   496   497   Cleavage (by kallikrein).
FT   MOD_RES   19   19   Pyrrolidone carboxylic acid.
FT   MOD_RES   380   380   4-hydroxyproline (By similarity).
FT   CARBOHYD   87   87   N-linked (GlcNAc...).
FT   CARBOHYD   136   136   N-linked (GlcNAc...); partial.
FT   CARBOHYD   168   168   N-linked (GlcNAc...).
FT   CARBOHYD   169   169   N-linked (GlcNAc...).
FT   CARBOHYD   197   197   N-linked (GlcNAc...); partial.
FT   CARBOHYD   204   204   N-linked (GlcNAc...).
FT   CARBOHYD   280   280   N-linked (GlcNAc...).
FT   CARBOHYD   396   396   O-linked (GalNAc...).
FT   CARBOHYD   397   397   O-linked (GalNAc...).
FT   CARBOHYD   398   398   O-linked (GalNAc...).
FT   CARBOHYD   400   400   O-linked (GalNAc...).
FT   CARBOHYD   404   404   O-linked (GalNAc...).
FT   CARBOHYD   510   510   O-linked (GalNAc...).
FT   CARBOHYD   518   518   O-linked (GalNAc...).
FT   CARBOHYD   522   522   O-linked (GalNAc...).
FT   CARBOHYD   534   534   O-linked (GalNAc...).
FT   CARBOHYD   546   546   O-linked (GalNAc...).
FT   CARBOHYD   551   551   O-linked (GalNAc...).
FT   CARBOHYD   568   568   O-linked (GalNAc...).
FT   CARBOHYD   589   589   O-linked (GalNAc...).
FT   DISULFID   27   568   Interchain (between heavy and light
FT   chain).
FT   DISULFID   228   247
FT   DISULFID   205   217
FT   DISULFID   141   144
FT   DISULFID   106   125
FT   DISULFID   82   93
FT   VARSPLIC   399   434   Missing (in isoform LMW).
FT   /FTId=VSP_013565.
FT   VARSPLIC   435   619   VSLPHSAMSPVQDEERDSGKEQGPTHGHGWDHGKQI -> T
FT   HVKSCEYKGRPEQEAGAEPAPQGEVSLPAESPQLAR (in
FT   isoform LMW).
FT   /FTId=VSP_013564.
FT   VARIANT   398   398   T -> P.
FT   VARIANT   401   401   T -> V.
FT   VARIANT   454   454   H -> K.
SQ   SEQUENCE   619 AA; 68710 MW; F04320A8EB0EE0DA CRC64;

Query Match   67.2%; Score 450; DB 1; Length 619;
Best Local Similarity   68.9%; Pred. No. 1.6e-33;
Matches   84; Conservative   14; Mismatches   22; Indels   2; Gaps   1;

Qy   3 GKDFVQPPTKICVGPCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
              ||:|||:||:|||||||||||||||||||||||||||:|||||||||||||||||:|||||
Db   252 GEDFL--PPMVCVGPCKPIPVDSPDLEBALNHSIAKLNAEHDGTFYFKIDTVKKATVQVV 309

Qy   63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   310 GGLKYSIVFIARETTCSKGSNEELTKSCEINHGQILHCDANYVYVPWEEKVYPTVNCQP 369

Qy   123 LG 124
              ||
Db   370 LG 371

RESULT 6
ID   Q6S911_MOUSE   PRELIMINARY;   PRT;   480 AA.
AC   Q6S911;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   HMW kininogen-I variant (High molecular weight kininogen I isoform
DE   DeltaD5).
GN   Name=Kng1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RP   STRAIN=FVB/N;
RX   MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA   Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,
RA   Bader M.;
RT   "Structure and expression of two kininogen genes in mice.";
RL   Biol. Chem. 385:295-301(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RP   STRAIN=C57BL;
RA   Merkulov S.M., Komar A.A., McCrae K.R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY462058; AAR88632.1; -; mRNA.
DR   EMBL; AY605571; AAT00087.1; -; mRNA.
DR   MGI; MGI:1097705; Kng1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 1.
SQ   SEQUENCE   480 AA; 53205 MW; 7D0AE95FC5AA98DE CRC64;

Query Match   64.8%; Score 434; DB 2; Length 480;
Best Local Similarity   66.1%; Pred. No. 3.8e-32;
Matches   82; Conservative   11; Mismatches   31; Indels   0; Gaps   0;

Qy   2 SGKDFVQPPTKICVGPCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV 61
              |:||||||||:|||:|||||||||||||||:|:|||||||||||||||||||||||:|||:
Db   251 SGDDLVEALPKPCPGCPRDIPVDSPELKEVLGHSIAQLNAENDHPFYYKIDTVKKATSQV 310

Qy   62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQ 121
              ||||:||||||||||||||||||||||||||||||||:|||||:||||:||||||||||||
Db   311 VAGTKYVIEFIARETKCSKESNTELAEDCEIKHLGQSLDCNANVYMRPWENKVVPTVRCKQ 370

Qy   122 PLGM 125
              ||||
Db   371 ALDM 374

RESULT 7
ID   KNG1_MOUSE   STANDARD;   PRT;   661 AA.
AC   O08677; O08676; Q91XK5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Kininogen-1 precursor [Contains: Kininogen-1 heavy chain; Bradykinin;
DE   Kininogen-1 light chain].
GN   Name=Kng1; Synonyms=Kng;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS HMW AND LMW).
RP   STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX   MEDLINE=97342556; PubMed=9199253; DOI=10.1016/S0167-4781(97)00018-3;
RA   Takano M., Kondo J., Yayama K., Otani M., Sano K., Okamoto H.;
RT   "Molecular cloning of cDNAs for mouse low-molecular-weight and high-
RT   molecular-weight prekininogens.";
RL   Biochim. Biophys. Acta 1352:222-230(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LMW).
RP   STRAIN=C57BL/6J; TISSUE=Placenta;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nishi I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA   Yagi K., Tomaru Y., Haaegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LMW).
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
CC   HMW-kininogen plays an important role in blood coagulation by
CC   helping to position optimally prekallikrein and factor XI next to
CC   factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-
CC   induced aggregation of thrombocytes; (4) the active peptide
CC   bradykinin that is released from HMW-kininogen shows a variety of
CC   physiological effects: (4A) influence in smooth muscle
CC   contraction, (4B) induction of hypotension, (4C) natriuresis and
CC   diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC   mediator of inflammation and causes (4E1) increase in vascular
CC   permeability, (4E2) stimulation of nociceptors (4E3) release of
CC   other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC   a cardioprotective effect (directly via bradykinin action)
CC   indirectly via endothelium-derived relaxing factor action); (5)
CC   LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC   kininogen is in contrast to HMW-kininogen not involved in blood
CC   clotting (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=HMW;
CC   IsoId=O08677-1; Sequence=Displayed;

CC   Name=LMW;
CC   IsoId=O08677-2; Sequence=VSP_001263, VSP_001264;
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC   -!- SIMILARITY: Contains 3 cystatin-like domains.
CC   --

DR   EMBL; D84435; BAA19743.1; -; mRNA.
DR   EMBL; D84415; BAA19742.1; -; mRNA.
DR   EMBL; AK005547; -; NOT ANNOTATED CDS; mRNA.
DR   EMBL; BC018158; AAH18158.1; -; mRNA.
DR   Ensembl; ENSMUSG00000022875; Mus musculus.
DR   MGI; MGI:1097705; Kng1.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00334; KININOGEN.
DR   PROSITE; PS00287; CYSTATIN; 1.
KW   Alternative splicing; Blood coagulation; Bradykinin; Glycoprotein;
KW   Inflammatory response; Plasma; Protease inhibitor; Repeat; Signal;
KW   Thiol protease inhibitor; Vasoactive; Vasodilator.
FT   SIGNAL   1   18   Potential.
FT   CHAIN   19   661   Kininogen-1.
FT   CHAIN   19   379   Kininogen-1 heavy chain.
FT   PEPTIDE   380   388   Bradykinin.
FT   CHAIN   389   661   Kininogen-1 light chain.
FT   DOMAIN   19   135   Cystatin-like 1.
FT   DOMAIN   136   257   Cystatin-like 2.
FT   DOMAIN   258   379   Cystatin-like 3.
FT   COMPBIAS   439   524   His-rich.
FT   CARBOHYD   82   82   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   168   168   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   204   204   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   242   242   N-linked (GlcNAc...) (Potential).
FT   DISULFID   28   631   Interchain (between heavy and light
FT   chains) (By similarity).
FT   DISULFID   83   94   By similarity.
FT   DISULFID   107   125   By similarity.
FT   DISULFID   141   144   By similarity.
FT   DISULFID   205   217   By similarity.
FT   DISULFID   228   247   By similarity.
FT   DISULFID   263   266   By similarity.
FT   DISULFID   327   339   By similarity.
FT   DISULFID   350   369   By similarity.
FT   VARSPLIC   401   432   VSPPYIAREQEERDAETEQGPTHGWLHEKQ -> RLLRA
FT   CBYKGRLSKAGAEPAPERQAESSQVKQ (in isoform
FT   LMW).
FT   /FTId=VSP_001263.
FT   VARSPLIC   433   661   Missing (in isoform LMW).
FT   /FTId=VSP_001264.
SQ   SEQUENCE   661 AA; 73102 MW; 77446025BD587956 CRC64;

Query Match   64.8%; Score 434; DB 1; Length 661;
Best Local Similarity   66.1%;
Matches   82; Conservative   11; Mismatches   31; Indels   0; Gaps   0;

Qy   2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKARVQV 61
              || | | || ||||||| |||| | || | |||||| | |||| |||| ||
Db   251 SGDDLVEALPKPCPGCPRDIPVDSPELKEVLGHSIAQLNAENDHPFYKIDTVKKATSQV 310

Qy   62 VAGKKYFPIDFVARETTCSKESNEELTESCETFKKLGQSLDCNAEVYVVPWEKKIYPTVNCQ 121
              ||| | | |||||| |||||| || | | | |||||||||| | ||| | |||| ||
Db   311 VAGTKVVIEFIARETKCSKESNTELAEDCEIKHLGQSLDCNANVMRPWENKVVPTVKCQ 370

Qy   122 PLGM 125
              ||
Db   371 ALDM 374

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RESULT 8
ID   Q5M8A0_RAT     PRELIMINARY;      PRT;   433 AA.
AC   Q5M8A0;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Kng1 protein.
GN   Name=Kng1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC088155; AAH88155.1; -; mRNA.
DR   GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
SQ   SEQUENCE   433 AA;   47891 MW;  6D58434855166ED CRC64;

     Query Match             63.6%;
     Best Local Similarity   65.0%;
     Matches   80;  Conservative   14;  Mismatches   29;  Indels   0;  Gaps   0;

Qy          3  GKDFVQPPTKICVGCPRDIPTNSPELEETLLTHTITKLNAENNATFYFKIDNVKKARVQVV   62
               |||| ||| | |: ||||: |:||:| :| |||||||||:||||: |:||:|:|:|:|||
Db        253  GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTFYFKIDTVKKATSQVV   312

Qy         63  AGKKYFIDFVARETTCSKESNEELTESCETTKXLQGSLDCNAEVYVVPWEKKIYPTVNCQP  122
               || | ||:| ||| ||:|:| :| :| | |||:|:|||| ||:| |:|::| |:| |
Db        313  AGTKVYEFIARETKCSKESNABLTADCETKRLGQSLNCNANVYMRFWENKVVPTVCCKV   372


RESULT 9
ID   KNG1_RAT      STANDARD;      PRT;   639 AA.
AC   P08934; P08933;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Kininogen-1 precursor (Contains: Kininogen-1 heavy chain; Bradykinin;
DE   Kininogen-1 light chain).
GN   Name=Kng1; Synonyms=Kng;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS HMW AND LMW).
RX   MEDLINE=87137443; PubMed=3029068;
RA   Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
RT   "Differing expression patterns and evolution of the rat kininogen gene
RT   family.";
RL   J. Biol. Chem. 262:2190-2198(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RA   Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT   "Primary structures of the mRNAs encoding the rat precursors for
RT   bradykinin and T-kinin. Structural relationship of kininogens with
RT   major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
RL   J. Biol. Chem. 260:12054-12059(1985).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-65.
RC   STRAIN=Buffalo;
RX   MEDLINE=86008264; PubMed=2413018;
RA   Fung W.-P., Schreiber G.;
RT   "Structure and expression of the genes for major acute phase alpha 1-
RT   protein (thiostatin) and kininogen in the rat.";
RL   J. Biol. Chem. 262:9298-9308(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 1-41.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=87250580; PubMed=2439509;
RA   Kageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
RT   "Differing utilization of homologous transcription initiation sites of
RT   rat K and T kininogen genes under inflammation condition.";
RL   J. Biol. Chem. 262:2345-2351(1987).
CC   -!- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
CC       HMW-kininogens plays an important role in blood coagulation by
CC       helping to position optimally prekallikrein and factor XI next to
CC       factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-
CC       induced aggregation of thrombocytes; (4) the active peptide
CC       bradykinin that is released from HMW-kininogen shows a variety of
CC       physiological effects: (4A) influence in smooth muscle
CC       contraction; (4B) induction of hypotension; (4C) natriuresis and
CC       diuresis; (4D) decrease in blood glucose level; (4E) it is a
CC       mediator of inflammation and causes (4E1) increase in vascular
CC       permeability, (4E2) stimulation of nociceptors (4E3) release of
CC       other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC       a cardioprotective effect (directly via bradykinin action),
CC       indirectly via endothelium-derived relaxing factor action); (5)
CC       LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC       kininogen is in contrast to HMW-kininogen not involved in blood
CC       clotting.
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=HMW;
CC         IsoId=P08934-1; Sequence=Displayed;
CC       Name=LMW;
CC         IsoId=P08934-2; Sequence=VSP_001265, VSP_001266;
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
CC   -!- MISCELLANEOUS: Rats express four types of kininogens: the
CC       classical HMW/LMW kininogens and two additional LMW-like
CC       kininogens: T-I and T-II.
CC   -!- SIMILARITY: Contains 3 cystatin-like domains.
```

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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; L29428; AAA41486.1; -; mRNA.
DR   EMBL; M11884; AAA41487.1; -; mRNA.
DR   EMBL; M14369; AAA41484.1; -; Genomic_DNA.
DR   EMBL; M14369; AAA41485.1; -; Genomic_DNA.
DR   EMBL; M16455; AAA41482.1; -; ALT_SEQ; Genomic_DNA.
DR   PIR; A25486; A25486.
DR   PIR; A28055; A28055.
DR   HSSP; P01040; 1DVD.
DR   RGD; 2980; kng1.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   InterPro; IPR003243; Prot_inh_I25A_B.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00334; KININOGEN.
DR   ProDom; PD001231; Prot_inh_I25A_B; 1.
DR   PROSITE; PS02287; CYSTATIN; 2.
DR   PROSITE; PS00287; CYSTATIN; 1.
KW   Alternative splicing; Blood coagulation; Bradykinin; Glycoprotein;
KW   Inflammatory response; Multigene family; Plasma; Protease inhibitor;
KW   Repeat; Signal; Thiol protease inhibitor; Vasoactive; Vasodilator.
FT   SIGNAL        1     18
FT   CHAIN        19    639       Kininogen-1.
FT   CHAIN        19    380       Kininogen-1 heavy chain.
FT   PEPTIDE     381    389       Bradykinin.
FT   CHAIN       390    639       Kininogen-1 light chain.
FT   DOMAIN       19    136       Cystatin-like 1.
FT   DOMAIN      137    258       Cystatin-like 2.
FT   DOMAIN      259    380       Cystatin-like 3.
FT   DOMAIN      439    514       His-rich.
FT   COMPBIAS    439    514       His-rich.
FT   CARBOHYD     82     82       N-linked (GlcNAc...).     (Potential).
FT   CARBOHYD    127    127       N-linked (GlcNAc...).     (Potential).
FT   CARBOHYD    169    169       N-linked (GlcNAc...).     (Potential).
FT   CARBOHYD    205    205       N-linked (GlcNAc...).     (Potential).
FT   CARBOHYD    294    294       N-linked (GlcNAc...).     (Potential).
FT   CARBOHYD    529    529       N-linked (GlcNAc...).     (Potential).
FT   DISULFID     28    609       Interchain (between heavy and light
FT                                chains) (By similarity).
FT   DISULFID     83     94       By similarity.
FT   DISULFID    107    126       By similarity.
FT   DISULFID    142    145       By similarity.
FT   DISULFID    206    218       By similarity.
FT   DISULFID    229    248       By similarity.
FT   DISULFID    264    267       By similarity.
FT   DISULFID    328    340       By similarity.
FT   DISULFID    351    370       By similarity.
FT   VARSPLIC    402    433       VSPSYIARVQBERDPGNEQSPIHGHGWLHAKQ -> RLLNS
FT                                CEYKGRLLKAGAGPAPERQAEASTVTP (in isoform
FT                                LMW).
FT   VARSPLIC    434    639       Missing (in isoform LMW).
FT                                /FTId=VSP_001265.
FT                                /FTId=VSP_001266.
FT   CONFLICT     61     61       E -> K (in Ref. 2).
SQ   SEQUENCE   639 AA;  70933 MW;  D3172DF94FF56AF5 CRC64;

Query Match             63.6%;  Score 426;  DB 1;  Length 639;
Best Local Similarity   65.0%;  Pred. No. 2.9e-31;
Matches   80;  Conservative   14;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTTKLNAENNATFYFKIDNVKKARVQVV 62
                ||  | |||||:|:|||||||:||||||||:||| ||||||||||||||||||||||||||
Db        253 GDDLPFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTFYFKIDTVKKATSQVV 312

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||:
Db        313 AGTKYVIEFIARETKCSKESNAELTADCETKRLGQSLNCNANVYMRPWENKVIPTVKCKV 372

Qy        123 LGM 125
                |||
Db        373 LDM 375
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RESULT 10
Q6S9I0_MOUSE
ID   Q6S9I0_MOUSE PRELIMINARY;      PRT;   433 AA.
AC   Q6S9I0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LMW kininogen-II.
GN   Name=Kng2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RX   MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA   Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,
RA   Bader M.;
RT   "Structure and expression of two kininogen genes in mice.";
RL   Biol. Chem. 385:295-301(2004).
DR   MGI; MGI:3027157; Kng2.
DR   EMBL; AY462059; AAR88633.1; -; mRNA.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 1.
SQ   SEQUENCE   433 AA;  47887 MW;  C86F7BE91C7FE9C0 CRC64;

Query Match             63.4%;  Score 425;  DB 2;  Length 433;
Best Local Similarity   66.1%;  Pred. No. 2.4e-31;
Matches   80;  Conservative   10;  Mismatches   31;  Indels    0;  Gaps    0;

Qy          3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTTKLNAENNATFYFKIDNVKKARVQVV 62
                ||  | ||||||:|||||||||:||||||:||||:||| ||||||:|||||||||||||
Db        252 GDDLVEALPKPCPGCPRDIPVDSPELKEVLGHSIAQLNTENDHPFYFKIDLVKKATSQVV 311

Qy         63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 122
                |||||||||||||||||||||||||||||:||||||||||||:||| || ||:|||||:
Db        312 AGTNYVIEFIARETKCSKESNTELTEDCEIKHLGQSLDCNANVYMRPWENKVIPTVKCQA 371

Qy        123 L 123
                |
Db        372 L 372
```

```
RESULT 11
Q6S9I2_MOUSE
ID   Q6S9I2_MOUSE PRELIMINARY;      PRT;   462 AA.
AC   Q6S9I2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HMW-kininogen-II variant.
GN   Name=Kng2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RX   MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA   Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,
RA   Bader M.;
RT   "Structure and expression of two kininogen genes in mice.";
RL   Biol. Chem. 385:295-301(2004).
DR   MGI; MGI:3027157; Kng2.
DR   EMBL; AY462057; AAR88631.1; -; mRNA.
DR   GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
```

```
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 1.
SQ   SEQUENCE   462 AA;  51052 MW;  2A921AB50741C1DC CRC64;

Query Match             63.4%;  Score 425;  DB 2;  Length 462;
Best Local Similarity   66.1%;  Pred. No. 2.5e-31;
Matches   80;  Conservative   10;  Mismatches   31;  Indels   0;  Gaps   0;

Qy         3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
             ||||| ||| :|| ||||||||||  ||| ||| |: :|| ||| |||||||| |||
Db       252 GDDLVEALPKPCPGCPRDIPVDSPELKEVLGHSIAQLNTENDHPPYFKIDTVKKATSQVV 311

Qy        63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVYVVPWEKKIYPTVNCQP 122
             |||| ||| | :|||||| |||||| || || || || |||:|||||| |||||||||
Db       312 AGTNYVIEFIARETKCSKSNTELTEDCEIKHLGQSLDCNANVYMRPWENKVIPTVKCQA 371

Qy       123 |  123
             |
Db       372 L  372
```

```
RESULT 12
Q6S913_MOUSE
ID   Q6S913_MOUSE    PRELIMINARY;      PRT;   644 AA.
AC   Q6S913;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HMW kininogen-II.
GN   Name=Kng2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RX   MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA   Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,
RA   Bader M.;
RT   "Structure and expression of two kininogen genes in mice.";
RL   Biol. Chem. 385:295-301(2004).
DR   EMBL; AY462056; AAR88630.1; -; mRNA.
DR   MGI; MGI:3027157; Kng2.
DR   GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   Pfam; PF00031; Cystatin; 3.
DR   PRINTS; PR00334; KININOGEN.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 1.
SQ   SEQUENCE   644 AA;  71272 MW;  520A4B83114F565B CRC64;

Query Match             63.4%;  Score 425;  DB 2;  Length 644;
Best Local Similarity   66.1%;  Pred. No. 3.6e-31;
Matches   80;  Conservative   10;  Mismatches   31;  Indels   0;  Gaps   0;

Qy         3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
             ||||| ||| :|| ||||||||||  ||| ||| |: :|| ||| |||||||| |||
Db       252 GDDLVEALPKPCPGCPRDIPVDSPELKEVLGHSIAQLNTENDHPPYFKIDTVKKATSQVV 311

Qy        63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVYVVPWEKKIYPTVNCQP 122
             |||| ||| | :|||||| |||||| || || || || |||:|||||| |||||||||
Db       312 AGTNYVIEFIARETKCSKSNTELTEDCEIKHLGQSLDCNANVYMRPWENKVIPTVKCQA 371

Qy       123 |  123
             |
Db       372 L  372
```

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RESULT 13
KNT2_RAT
ID   KNT2_RAT        STANDARD;      PRT;   430 AA.
AC   P08932;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-FEB-2005 (Rel. 46, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
DE   (Thiostatin) [Contains: T-kininogen II heavy chain; T-kinin; T-
DE   kininogen II light chain].
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86008264; PubMed=2413018;
RA   Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT   "Primary structures of the mRNAs encoding the rat precursors for
RT   bradykinin and T-kinin. Structural relationship of kininogens with
RT   major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
RL   J. Biol. Chem. 260:12054-12059(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 5-430, AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=86008266; PubMed=2413019;
RA   Anderson K.P., Heath E.C.;
RT   "The relationship between rat major acute phase protein and the
RT   kininogens.";
RL   J. Biol. Chem. 260:12065-12071(1985).
-!- FUNCTION: Kininogens are plasma glycoproteins with a number of
    functions: (1) as precursor of the active peptide bradykinin they
    effect smooth muscle contraction, induction of hypotension and
    increase of vascular permeability. (2) They play a role in blood
    coagulation by helping to position optimally prekallikrein and
    factor XI next to factor XII. (3) They are inhibitor of thiol
    proteases.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Plasma.
-!- INDUCTION: In response to an inflammatory stimulant. T-kininogen
    II synthesis is induced and the plasma concentration of T-
    kininogen I is raised.
-!- PTM: As T-kinin is preceded by a Met instead of an Arg or Lys, it
    is not released from its precursor by either tissue or plasma
    kallikrein.
-!- MISCELLANEOUS: Rats express four types of kininogens: the
    classical HMW and LMW kininogens produced by alternative splicing
    of the same gene, and two additional LMW-like kininogens: T-I and
    T-II.
-!- SIMILARITY: Contains 3 cystatin-like domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
    in positions 180 and 181.
-------------------------------------------------------------------------
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-------------------------------------------------------------------------
DR   EMBL; M11885; AAA41491.1; -; mRNA.
DR   EMBL; M11661; AAA41570.1; ALT_FRAME; mRNA.
DR   PIR; B28055; B28055.
DR   GlycoSuiteDB; P08932; -.
DR   Ensembl; ENSRNOG00000003387; Rattus norvegicus.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   InterPro; IPR003243; Prot_inh_I25A_B.
DR   Pfam; PF00031; Cystatin; 3.
DR   ProDom; PD001231; Prot_inh_I25A_B; 1.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
KW   Acute phase; Bradykinin; Direct protein sequencing; Glycoprotein;
KW   Multigene family; Plasma; Protease inhibitor; Repeat; Signal;
KW   Thiol protease inhibitor; Vasoactive; Vasodilator.
```

```
FT   SIGNAL        1     18
FT   CHAIN        19    430       T-kininogen II.
FT   CHAIN        19    375       T-kininogen II heavy chain.
FT   PEPTIDE     376    386       T-kinin.
FT   CHAIN       387    430       T-kininogen II light chain.
FT   DOMAIN       19    135       Cystatin-like 1.
FT   DOMAIN      136    257       Cystatin-like 2.
FT   DOMAIN      258    375       Cystatin-like 3.
FT   CARBOHYD     82     82       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    126    126       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    168    168       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    204    204       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    326    326       N-linked (GlcNAc...)   (Potential).
FT   DISULFID     28    404       Interchain (between heavy and light
FT                                chain) (By similarity).
FT   DISULFID     83     94       By similarity.
FT   DISULFID    107    125       By similarity.
FT   DISULFID    141    144       By similarity.
FT   DISULFID    205    217       By similarity.
FT   DISULFID    228    247       By similarity.
FT   DISULFID    263    266       By similarity.
FT   DISULFID    327    339       By similarity.
FT   DISULFID    350    369       By similarity.
FT   CONFLICT     26     26       MD -> LN (in Ref. 1).
FT   CONFLICT     28     28       C -> R (in Ref. 2).
FT   CONFLICT     55     55       L -> V (in Ref. 1).
FT   CONFLICT     61     61       E -> K (in Ref. 1).
FT   CONFLICT    166    166       F -> S (in Ref. 1).
FT   CONFLICT    179    179       T -> I (in Ref. 1).
FT   CONFLICT    193    193       N -> D (in Ref. 2).
FT   CONFLICT    212    212       R -> T (in Ref. 1).
FT   CONFLICT    229    229       F -> S (in Ref. 1).
FT   CONFLICT    233    233       A -> L (in Ref. 1).
FT   CONFLICT    415    415       Y -> H (in Ref. 2).
SQ   SEQUENCE    430 AA;  47704 MW;  D94628D848C81525 CRC64;
```

Qy   Query Match   61.0%;   Score 409;   DB 1;   Length 430;
      Best Local Similarity   61.8%;   Pred. No. 7.4e-30;
      Matches   76;   Conservative   15;   Mismatches   32;   Indels   0;   Gaps   0;

```
Qy      3  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV   62
           |||||:||||||||||||||||:|||:||:|||||::|:|||:|||:|||:||||||||
Db    252  GDDLFSLLPKKCFGCPKNIPVDSPELKEALGHSIAQLNAQHNHLFYFKIDTVKKATSQVV  311

Qy     63  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP  122
           ||||:|||:|||||||||::||||:|||||||||||||||:||:|||:||:|||||||||
Db    312  AGTKVIEFIARETNCSKQTNTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA   371

Qy    123  LGM  125
           |||
Db    372  LDM  374
```

RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Director MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081161; AAH88161.1; -; mRNA.
DR   GO; GO:0048869; F:cysteine protease inhibitor activity; IEA.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   InterPro; IPR003243; Prot_inh_I25A_B.
DR   Pfam; PF00031; Cystatin; 3.
DR   ProDom; PD001231; Prot_inh_I25A_B; 1.
DR   SMART; SM00043; CY; 3.
DR   PROSITE; PS00287; CYSTATIN; 2.
SQ   SEQUENCE   430 AA; 47704 MW; D94628D848C81525 CRC64;

Qy   Query Match   61.0%;   Score 409;   DB 2;   Length 430;
      Best Local Similarity   61.8%;   Pred. No. 7.4e-30;
      Matches   76;   Conservative   15;   Mismatches   32;   Indels   0;   Gaps   0;

```
Qy      3  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV   62
           |||||:||||||||||||||||:|||:||:|||||::|:|||:|||:|||:||||||||
Db    252  GDDLFSLLPKKCFGCPKNIPVDSPELKEALGHSIAQLNAQHNHLFYFKIDTVKKATSQVV  311

Qy     63  AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP  122
           ||||:|||:|||||||||::||||:|||||||||||||||:||:|||:||:|||||||||
Db    312  AGTKVIEFIARETNCSKQTNTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA   371

Qy    123  LGM  125
           |||
Db    372  LDM  374
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RESULT 14
ID   Q5M894_RAT   PRELIMINARY;   PRT;   430 AA.
AC   Q5M894;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Similar to alpha-1 major acute phase protein prepeptide.
GN   Name=MGC108747;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RESULT 15
ID   Q7YRP6_PIG   PRELIMINARY;   PRT;   140 AA.
AC   Q7YRP6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Low molecular weight kininogen (Fragment).
GN   Name=kng;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=13679312; DOI=10.1095/biolreprod.103.020412;
RA   Vonnahme K.A., Fernando S.C., Ross J.W., Ashworth M.D., DeSilva U.,
RA   Malayer J.R., Geisert R.D.;
RT   "Porcine endometrial expression of kininogen, factor XII, and plasma
RT   kallikrein in cyclic and pregnant gilts.";
RL   Biol. Reprod. 70:132-138(2004).
DR   EMBL; AY321363; AAP85260.1; -; mRNA.

```
DR   HSSP; P01038; 1A90.
DR   GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR   InterPro; IPR000010; Prot_inh_cystat.
DR   InterPro; IPR003243; Prot_inh_I25A_B.
DR   Pfam; PF00031; Cystatin; 1.
DR   ProDom; PD001231; Prot_inh_I25A_B; 1.
DR   SMART; SM00043; CY; 1.
FT   NON_TER       1
FT   NON_TER     140
SQ   SEQUENCE    140 AA;  15650 MW;  1778378636603F777 CRC64;
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Query Match               60.3%;  Score 404;  DB 2;  Length 140;
Best Local Similarity     78.2%;  Pred. No. 6.4e-30;
Matches  79; Conservative  5; Mismatches 17; Indels  0; Gaps  0;

Qy   24 NSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN 83
         :|:.|:|| |:|:||||||||| |  :|| |||||  :||||||||||| |||||||:||
Db    1 DSPDLEEPLNHSIAKLNAENNAVFYFKIGPVEKATVQVVAGKKYSIVFTARETTCSKQSN 60

Qy   84 EELTESCETKKLGQSLDCNAEVTYVPWEKKIYPTVNCQPLG 124
         |||||||:|||||| :|| ||||| ||||||||||||  ||
Db   61 EELTESCEIKKPGQILKCNASVYVVPWEKKIYPTVKCQLLG 101
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Search completed: February 8, 2006, 03:17:09
Job time : 254 secs